



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 142047

To: Jeffrey Parkin
Location: rem/3d39/3c18
Art Unit: 1648
Friday, January 21, 2005

Case Serial Number: 10/085944

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

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From: *72607* Parkin, Jeffrey
Sent: Friday, January 07, 2005 9:05 PM
To: STIC-Biotech/ChemLib
Subject: Sequence Search for U.S. Serial No. 10/085,944

Would you please search **SEQ ID NO.: 2** from the aforementioned application (U.S. Serial No. 10/085,944; Wang, W.) v. all relevant **PUBLIC/COMMERCIAL** databases.

Place results on **PAPER**.

Please include the first **50 SUMMARIES**.

Thanks!

JSP
AU 1648
REM 3D39
2-0908

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____

Searcher: *Beverly e 2528*

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors:

_____ IG
_____ *L* STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ *✓* Other *CGN*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 11:23:36 ; Search time 938 Seconds

(without alignments)
1411.633 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatctgctgaacggagagaaaccgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	342	14	FLD2CPM2
2	28	100.0	840	14	AF360860 Dengue vi
3	28	100.0	840	14	AF360861 Dengue vi
4	28	100.0	840	14	AF360862 Dengue vi
5	28	100.0	840	14	AF360863 Dengue vi
6	28	100.0	2319	14	S66064 structural
7	28	100.0	2325	14	AF469175 Dengue vi
8	28	100.0	2325	14	AF469176 Dengue vi
9	28	100.0	2325	14	AF509530 Dengue vi
10	28	100.0	2325	14	AY044442 Dengue vi
11	28	100.0	2357	6	AR232496 Sequence
12	28	100.0	2357	14	DEN2NGC
13	28	100.0	2469	14	DEN2JMA
14	28	100.0	2552	14	AY152036S1
15	28	100.0	2552	14	AY152040S1
16	28	100.0	2552	14	AY152044S1
17	28	100.0	2552	14	AY152048S1
18	28	100.0	2552	14	AY152052S1
19	28	100.0	2552	14	AY152056S1

20	28	100.0	2552	14	AY152060S1	Dengue vi
21	28	100.0	2552	14	AY152064S1	Dengue vi
22	28	100.0	2552	14	AY152068S1	Dengue vi
23	28	100.0	2552	14	AY152072S1	Dengue vi
24	28	100.0	2552	14	AY152076S1	Dengue vi
25	28	100.0	2552	14	AY152080S1	Dengue vi
26	28	100.0	2552	14	AY152084S1	Dengue vi
27	28	100.0	2552	14	AY152088S1	Dengue vi
28	28	100.0	2552	14	AY152092S1	Dengue vi
29	28	100.0	2552	14	AY152096S1	Dengue vi
30	28	100.0	2552	14	AY152100S1	Dengue vi
31	28	100.0	2552	14	AY152104S1	Dengue vi
32	28	100.0	2552	14	AY152108S1	Dengue vi
33	28	100.0	2552	14	AY152112S1	Dengue vi
34	28	100.0	2552	14	AY152116S1	Dengue vi
35	28	100.0	2552	14	AY152120S1	Dengue vi
36	28	100.0	2552	14	AY152124S1	Dengue vi
37	28	100.0	2552	14	AY152128S1	Dengue vi
38	28	100.0	2552	14	AY152132S1	Dengue vi
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43	28	100.0	2552	14	AY152152S1	Dengue vi
44	28	100.0	2552	14	AY152156S1	Dengue vi
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46	28	100.0	2552	14	AY152164S1	Dengue vi
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49	28	100.0	2552	14	AY152176S1	Dengue vi
50	28	100.0	2552	14	AY152180S1	Dengue vi

ALIGNMENTS

RESULT 1
FLD2CPM2
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
CDS

FLD2CPM2
Dengue-2 virus RNA for capsid protein, partial, from a case of dengue shock syndrome (M2).
X51709
1 GI:59299
Dengue virus type 2
Dengue virus type 2
Flavivirus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; 1 (bases 1 to 342)
Samuel,S., Koh,C.L., Pang,T. and Lam,S.K.
Nucleotide and encoded amino acid sequences of the capsid protein gene of three dengue-2 viruses isolated in Malaysia from patients with dengue haemorrhagic fever, dengue shock syndrome or dengue fever
Nucleic Acids Res. 18 (7), 1904 (1990)
90245598
2336373
2 (bases 1 to 342)
Koh,C.L.
Direct Submission
Submitted (05-FEB-1990) Koh C.-L., University of Malaysia, Department of Genetics and Cellular Biology, 5910 Kuala Lumpur, Malaysia
See <M15075> and <M19197> for previously reported sequence. See <X51708> and <X51710> for capsid protein sequences of M1 and M3. Location/Qualifiers
1..342
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/mol_type="genomic RNA"
/strain="M2, isolated from case of dengue shock syndrome"
/db_xref="taxon:11060"
1..342
/note="unnamed protein product; capsid protein, partial

ORIGIN

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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAAACCGCG 28
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Db 40 AATATGCTGAAACGCGAGAAACCGCG 67
|||||

RESULT 2

AF360860

LOCUS

DEFINITION

840 bp ss-RNA linear VRL 11-FEB-2002

ACCESSION

AF360860

VERSION

AF360860.1 GI:18644121

KEYWORDS

Dengue virus type 2

SOURCE

ORGANISM

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

REFERENCE

1 (bases 1 to 840)

Uzcátegui, N.Y., Camacho, D., Comach, G., Cuello de Uzcátegui, R.,
Holmes, E.C. and Gould, E.A.
Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)

JOURNAL

MEDLINE

PUBMED

21571640

REFERENCE

2 (bases 1 to 840)

Uzcátegui, N.Y., Camacho, D., Comach, G., Cuello de Uzcátegui, R.,
Holmes, E.C. and Gould, E.A.
Direct Submission
Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
Oxford OX2 6UD, England

JOURNAL

LOCATION/Qualifiers

1. .840

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/isolate="LARD1432"

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/country="Venezuela"

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Db 40 AATATGCTGAAACGCGAGAAACCGCG 67
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RESULT 4

AF360862

LOCUS

DEFINITION

840 bp ss-RNA linear VRL 11-FEB-2002

ACCESSION

AF360862

VERSION

AF360862.1 GI:18644125

KEYWORDS

Dengue virus type 2

SOURCE

ORGANISM

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

REFERENCE

1 (bases 1 to 840)

Uzcátegui, N.Y., Camacho, D., Comach, G., Cuello de Uzcátegui, R.,
Holmes, E.C. and Gould, E.A.

JOURNAL

MEDLINE

PUBMED

21571640

REFERENCE

2 (bases 1 to 840)

Uzcátegui, N.Y., Camacho, D., Comach, G., Cuello de Uzcátegui, R.,
Holmes, E.C. and Gould, E.A.
Direct Submission
Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
Oxford OX2 6UD, England

JOURNAL

LOCATION/Qualifiers

1. .840

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

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/country="Venezuela"

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ORIGIN

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Db 40 AATATGCTGAAACGCGAGAAACCGCG 67

RESULT 3

AF360861

LOCUS

DEFINITION

840 bp ss-RNA linear VRL 11-FEB-2002

ACCESSION

AF360861

VERSION

AF360861.1 GI:18644123

KEYWORDS

Dengue virus type 2

SOURCE

ORGANISM

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

REFERENCE

1 (bases 1 to 840)

Uzcátegui, N.Y., Camacho, D., Comach, G., Cuello de Uzcátegui, R.,
Holmes, E.C. and Gould, E.A.
Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)

JOURNAL

MEDLINE

PUBMED

21571640

REFERENCE

2 (bases 1 to 840)

Uzcátegui, N.Y., Camacho, D., Comach, G., Cuello de Uzcátegui, R.,
Holmes, E.C. and Gould, E.A.
Direct Submission
Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
Oxford OX2 6UD, England

JOURNAL

LOCATION/Qualifiers

1. .840

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/isolate="LARD1701"

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/country="Venezuela"

1. .>840

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PSMT"

ORIGIN

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|||||

Db 40 AATATGCTGAAACGCGAGAAACCGCG 67
|||||

RESULT 4

AF360862

LOCUS

DEFINITION

840 bp ss-RNA linear VRL 11-FEB-2002

ACCESSION

AF360862

VERSION

AF360862.1 GI:18644125

KEYWORDS

Dengue virus type 2

SOURCE

ORGANISM

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

REFERENCE

1 (bases 1 to 840)

Uzcátegui, N.Y., Camacho, D., Comach, G., Cuello de Uzcátegui, R.,
Holmes, E.C. and Gould, E.A.

JOURNAL

MEDLINE

PUBMED

21571640

REFERENCE

2 (bases 1 to 840)

Uzcátegui, N.Y., Camacho, D., Comach, G., Cuello de Uzcátegui, R.,
Holmes, E.C. and Gould, E.A.
Direct Submission
Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
Oxford OX2 6UD, England

JOURNAL

LOCATION/Qualifiers

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ORIGIN

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Db 40 AATATGCTGAAACGCGAGAAACCGCG 67
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RESULT 4

AF360862

LOCUS

DEFINITION

840 bp ss-RNA linear VRL 11-FEB-2002

ACCESSION

AF360862

VERSION

AF360862.1 GI:18644125

KEYWORDS

Dengue virus type 2

SOURCE

ORGANISM

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

REFERENCE

1 (bases 1 to 840)

Uzcátegui, N.Y., Camacho, D., Comach, G., Cuello de Uzcátegui, R.,
Holmes, E.C. and Gould, E.A.

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TITLE      Molecular epidemiology of dengue type 2 virus in Venezuela:
JOURNAL    evidence for in situ virus evolution and recombination
MEDLINE    J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
PUBMED     21571640
REFERENCE  2 (bases 1 to 840)
AUTHORS    Uzategui,N.Y., Camacho,D., Comach,G., Cuello de Uzategui,R.,
           Holmes,E.C. and Gould,E.A.
TITLE      Direct Submission
JOURNAL    Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
           Oxford OX2 6UD, England
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DEFINITION
Dengue virus type 2 isolate LARD1996 polyprotein gene, partial cds.
ACCESSION AF360863
VERSION   AF360863.1 GI:18644127
KEYWORDS  Dengue virus type 2
SOURCE    Dengue virus type 2
            Organism: Dengue virus group.
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 840)
AUTHORS   Uzategui,N.Y., Camacho,D., Comach,G., Cuello de Uzategui,R.,
           Holmes,E.C. and Gould,E.A.
TITLE     Molecular epidemiology of dengue type 2 virus in Venezuela:
           evidence for in situ virus evolution and recombination
JOURNAL   J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
MEDLINE   21571640
PUBMED    11714970
REFERENCE 2 (bases 1 to 840)
AUTHORS   Uzategui,N.Y., Camacho,D., Comach,G., Cuello de Uzategui,R.,
           Holmes,E.C. and Gould,E.A.
TITLE     Direct Submission
JOURNAL   Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
           Oxford OX2 6UD, England
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TRTETWMSSEGAWKHVQRIETWILRHHPGFAIMAAILAYTIGTTHFQKALIFILLTAVA
PSMT"
ORIGIN
Query Match      100.0%; Score 28; DB 14; Length 840;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        |||||
        40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 6
LOCUS     S66064      2319 bp      DNA      linear      VRL 04-DEC-1993
DEFINITION
structural polyprotein [dengue type 4 virus DEN4, H241-P, Genomic,
2319 nt].
ACCESSION S66064
VERSION   S66064.1 GI:432575
KEYWORDS  Dengue virus type 4
SOURCE    Dengue virus type 4
            Organism: Dengue virus group.
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2319)
AUTHORS   Kawano,H., Rostashov,V., Rosen,L. and Lai,C.J.
TITLE     Genetic determinants of dengue type 4 virus neurovirulence for mice
JOURNAL   J. Virol. 67 (11), 6567-6575 (1993)
MEDLINE   94016840
PUBMED    8411360
REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gisseq 138430] from the original journal article.
FEATURES   Location/Qualifiers
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                        KMEKRLIKGMSYNTKMSGKSIDKEMASTQHGTTVVKYEGAGAPCKVPIRDNKE
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            ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64
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RESULT 7
AF469175
LOCUS
DEFINITION
Dengue virus type 2 strain GD24/93 polyprotein gene, partial cds.
ACCESSION
AF469175
VERSION
AF469175.1 GI:18766554
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2325)
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
Structural genes of dengue virus type 2 strain GD24/93 isolate from
Nanhai, Guangdong, China
Unpublished
2 (bases 1 to 2325)
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
Direct Submission
Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
Location/Qualifiers
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/codon_start=1
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TRTETWSSSEGAWKHAQRIETWILRHFGFTIMAILAYTITGTHFQRLAIFILITAVA
PSMTMRCIGISNRDFVEGSGSVWDIVLEHSGCVTTMAKNKPLDLELIKTEAKHPA
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RYVLGRITVNPVITERKSPVNIIEAPFGDSYIIIGVEPQLKLNWFKKSGSITGMWF
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67
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RESULT 8
AF469175
LOCUS
DEFINITION
Dengue virus type 2 polyprotein gene, partial cds.
ACCESSION
AF509530
VERSION
AF509530.1 GI:21070436
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

AF469176
LOCUS
DEFINITION
Dengue virus type 2 strain GD08/98 polyprotein gene, partial cds.
ACCESSION
AF469176
VERSION
AF469176.1 GI:18766556
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2325)
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
Structural genes of dengue virus type 2 strain GD24/93 isolate from
Nanhai, Guangdong, China
Unpublished
2 (bases 1 to 2325)
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
Direct Submission
Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
Location/Qualifiers
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/db_xref="GI:18766557"

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TRTETWSSSEGAWKHAQRIETWILRHFGFTIMAILAYTITGTHFQRLAIFILITAVA
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67
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RESULT 9
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LOCUS
DEFINITION
Dengue virus type 2 polyprotein gene, partial cds.
ACCESSION
AF509530
VERSION
AF509530.1 GI:21070436
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

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REFERENCE 1 (bases 1 to 2325)
AUTHORS Ren,R., Yu,F., Dong,T., Wei,L., Hua,J., Yan,H. and Peng,C.
TITLE Isolation, identification and sequence analyses of dengue virus
JOURNAL type 2 strain GD19/2001
Unpublished
REFERENCE 2 (bases 1 to 2325)
AUTHORS Ren,R., Yu,F., Dong,T., Wei,L., Hua,J., Yan,H. and Peng,C.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2002) Microbiology Department, The Military
Medical Institute of Guangzhou Military District, Dongguanhuang
Road, Guangzhou 510507, China
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Query Match 100.0%; Score 28; DB 14; Length 2325;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67

RESULT 10
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LOCUS Dengue virus type 2 strain Mar3 polyprotein gene, partial cds.
ACCESSION AY044442
VERSION AY044442.1 GI:18643733
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2325)
Uzcataguei.N.Y., Camacho,D., Cuello de Uzcataguei.R.,
Holmes,E.C. and Gould,E.A.
Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
21571640
MEDLINE 11714970
PUBMED
REFERENCE 2 (bases 1 to 2325)
Uzcataguei.N.Y., Camacho,D., Cuello de Uzcataguei.R.M.,
Holmes,E.C. and Gould,E.A.
Direct Submission
TITLE Submitted (09-JUL-2001) Flavivirus Group, CEH-Oxford, Mansfield
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Road, Oxford OX1 3SR, United Kingdom
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841..2325
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67

RESULT 11
AR232496 2357 bp RNA linear PAT 20-DEC-2002
LOCUS Sequence 1 from patent US 6455509.
DEFINITION AR232496
ACCESSION AR232496
VERSION AR232496.1 GI:27274633
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2357)
Kochel,T.J., Porter,K.R., Raviprakash,K., Hoffman,S.L. and
Hayes,C.G.
Dengue nucleic acid vaccines that induce neutralizing antibodies
Patent: US 6455509-A 1 24-SEP-2002;
JOURNAL Location/Qualifiers
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1 of 4
Dengue virus type 4 (DEN-4)
SOURCE
ORGANISM
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
AUTHORS Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
AUTHORS Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 15
LOCUS AY152040S1
DEFINITION Dengue virus type 4 D4.19_1998 polyprotein precursor, gene, partial
cda.
ACCESSION AY152040
VERSION AY152040.1
KEYWORDS GI:28170815
SEGMENT 1 of 4
SOURCE Dengue virus type 4 (DEN-4)
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
AUTHORS

TITLE Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
JOURNAL Selection-Driven Evolution of Emergent Dengue Virus
PUBLISHED Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
REFERENCE 12832629
AUTHORS 2 (bases 1 to 2552)
 Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
 Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology. University of Puerto Rico - Rio
 Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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 DB 37 AATATGCTGAACGCGAGAGAAACCGCG 64
RESULT 16
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LOCUS Dengue virus type 4 D4.19.1998 polyprotein precursor, gene, partial
DEFINITION cds.
ACCESSION AY152044
VERSION AY152044.1 GI:28170824
KEYWORDS 1 of 4
SEGMENT Dengue virus type 4 (DEN-4)
SOURCE Dengue virus type 4
ORGANISM Viruses; serNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Dengue virus group.
 1 (bases 1 to 2552)
 Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
 Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
 Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
 Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 17
AY152048S1
LOCUS
DEFINITION Dengue virus type 4 D4.14_1998 RNA linear VRL 29-SEP-2003
cds.
ACCESSION AY152048.1 GI:28170833
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
AUTHORS
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES Location/Qualifiers
source
1. .2552
/organism="Dengue virus type 4"
/mol_type="genomic RNA"

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/db_xref="taxon:11070"
/country="Puerto Rico"
/note="acronym: DEN-4"
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/note="contains core protein, matrix protein and envelope glycoprotein"
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ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 18
AY152052S1
LOCUS
DEFINITION Dengue virus type 4 D4.12_1998 polyprotein precursor, gene, partial cds.
ACCESSION AY152052.1 GI:28170842
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
AUTHORS
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES Location/Qualifiers
source
1. .2552
/organism="Dengue virus type 4"
/mol_type="genomic RNA"
/isolate="D4.12_1998"
/db_xref="taxon:11070"
/country="Puerto Rico"
/note="acronym: DEN-4"
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/note="contains core protein, matrix protein and envelope glycoprotein"

/codon_start=1
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/protein_id="AAN38339.1"
/db_xref="GI:28170849"
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TVTYKCPLLVNTPEPIDWCNLTSTWVYGTCTQSGRRERKRSVLTTPHSGMGLT
RAETWMSSEGAKHAQRVESILRNPGFALLAGFMAVMIQGTQRTVFFVLMMLVAP
SYNRCVGVGNRDFVEGSGGANVDLLEHGGCVTTMAQGRPTLDLFLTAKTAKVAL
LRTYCIASISNITATRCPTQGEPLKEEQDQYICRRDVVDRGNGCGGLFGKGV
VTCAKFCSGKITGNLQVLENLTVVTVVTHNGDTHAVGNDTSNHGVTATITPRSPV
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HWNKYRMVTFKVPKAKRQDVTVLGSGQEGAMHSLAGATEVDSGDGNHMFAGHLKCKV
RMEKLRIKMSYTWCSGKFSDKEMAEQHGCTTVVKVYEGAGAPCKVPIEIRDVNKE
KVGRVLSSTPLAENTNSVTNIELEPPGDSYIIVGVNSALTILHMFKSGSSIGKMF
STYRKAKMALIGETANDFGVGGGLFTSLGKAVHQVFGSVYTTMFGGVSWMIRILIGP
LVLWIGTNSRNTSMAMTICAVGGITLFLGTQADMGCVSVWSGRELKCGSGIFVVDN
VHTWTEQYKQFOPESPARLASAILNAHKDGVCGIRSTRLENVMWKQITNELN"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 19
AV152056S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS
DEFINITION
Dengue virus type 4 D4.17_1998 polyprotein precursor, gene, partial
cbs.
ACCESSION
AV152056
VERSION
AV152056.1 GI:28170851
i of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
1. .2552
/organism="Dengue virus type 4"
/mol_type="genomic RNA"
/isolate="D4.17 1998"
/db_xref="taxon:11070"
/country="Puerto Rico"
/note="acronym: DEN-4"
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glycoprotein"
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/protein_id="AAN38343.1"
/db_xref="GI:28170858"
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TLCLLIPVMAFHLSTRDGEPLMIVAKHERGPLLFTKTEGINKTILAMDLMGCEM

CDS

TVTYKCPLLVNTPEPIDWCNLTSTWVYGTCTQSGRRERKRSVLTTPHSGMGLT
RAETWMSSEGAKHAQRVESILRNPGFALLAGFMAVMIQGTQRTVFFVLMMLVAP
SYNRCVGVGNRDFVEGSGGANVDLLEHGGCVTTMAQGRPTLDLFLTAKTAKVAL
LRTYCIASISNITATRCPTQGEPLKEEQDQYICRRDVVDRGNGCGGLFGKGV
VTCAKFCSGKITGNLQVLENLTVVTVVTHNGDTHAVGNDTSNHGVTATITPRSPV
EVKLPDYGELTDCPEPSGIDFNEMILMKMKKTWLVHQRWFLDPLPWTAGADTSEV
HWNKYRMVTFKVPKAKRQDVTVLGSGQEGAMHSLAGATEVDSGDGNHMFAGHLKCKV
RMEKLRIKMSYTWCSGKFSDKEMAEQHGCTTVVKVYEGAGAPCKVPIEIRDVNKE
KVGRVLSSTPLAENTNSVTNIELEPPGDSYIIVGVNSALTILHMFKSGSSIGKMF
STYRKAKMALIGETANDFGVGGGLFTSLGKAVHQVFGSVYTTMFGGVSWMIRILIGP
LVLWIGTNSRNTSMAMTICAVGGITLFLGTQADMGCVSVWSGRELKCGSGIFVVDN
VHTWTEQYKQFOPESPARLASAILNAHKDGVCGIRSTRLENVMWKQITNELN"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 20
AV152060S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS
DEFINITION
Dengue virus type 4 D4.45_1998 polyprotein precursor, gene, partial
cbs.
ACCESSION
AV152060
VERSION
AV152060.1 GI:28170860
i of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
1. .2552
/organism="Dengue virus type 4"
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/db_xref="taxon:11070"
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/note="acronym: DEN-4"
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glycoprotein"
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/protein_id="AAN38347.1"
/db_xref="GI:28170867"

CDS

CDS

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STYRGAKMAILGTAWDFSGVGLFTSLGKAVHQVFGSVTTTFMGVSWMIRILIGF
LVLTWIGTNSRNTSMAMTCIAVGGITLFLGFTVQADMGCVWSGRELKCSGIFVVDN
VHTWTEQYKFQFESPARLASAILNAHKDGVCGIRSTTTRLENVMMKQITNELN"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 21
AY152064S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS
DEFINITION Dengue virus type 4 D4.47_1998 polyprotein precursor, gene, partial cds.

ACCESSION AY152064
VERSION AY152064.1 GI:28170869
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE 1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629

REFERENCE 2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers

FEATURES
source

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/country="Puerto Rico"
/note="acronym: DEN-4"
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/protein_id="AA138351.1"
/db_xref="GI:28170869"
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TVYKCPLLVNTPEPIDDCMNLSTVMVYGTCTQSGERREKRSVALTPHSGMGLT
RAETWMSSEGAKHAQVSWILRNPGFALLAGPMAYIGQTLQRTVFFVLMVLAP
SYNRCVGNRDFVEGSGGAWDLVLEHGGCVTTWAQGRPTLDFELIKTTAKEVAL
LRTYCEASISNTIATRCPTQGEPLKEQDQOYICRRVDVRGNGWGCGLFGKGV
VTCAKFSGSKITGNLVQIENLYVTVVVTHNGDTHAVGNDTSHGVTATITPRSPV
EVKLDPYCGELTDCPEPSGIDFNEMILMKMKKTWLHKQWFLDPLPWTAGADTSEV
HNNYKERMVTFKVPKHAQDVTVLGSQEGAMHSALAGATEVSDGDNHMFAGHLKCKV
RVGRVISTPLAENTNSVTNIELEPPFGDSYIVIGVNSALTTLHWRKSSIGRMFE
STYRGAKMAILGTAWDFSGVGLFTSLGKAVHQVFGSVTTTFMGVSWMIRILIGF
LVLTWIGTNSRNTSMAMTCIAVGGITLFLGFTVQADMGCVWSGRELKCSGIFVVDN
VHTWTEQYKFQFESPARLASAILNAHKDGVCGIRSTTTRLENVMMKQITNELN"

CDS

100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 22
AY152068S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS
DEFINITION Dengue virus type 4 D4.13_1998 polyprotein precursor, gene, partial cds.

ACCESSION AY152068
VERSION AY152068.1 GI:28170878
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE 1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629

REFERENCE 2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers

source

1..2552
/organism="Dengue virus type 4"
/mol_type="genomic RNA"
/isolate="D4.13_1998"
/db_xref="taxon:11070"
/country="Puerto Rico"
/note="acronym: DEN-4"
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/product="polyprotein precursor"
/protein_id="AA138351.1"
/db_xref="GI:28170885"

CDS

100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

[illegible]

RESULT 23	AY152072S1	2552 bp	RNA	linear	VRL 29-SEP-2003
LOCUS	AY152072S1				
DEFINITION	Dengue virus type 4 D4.46_1998 polyprotein precursor, gene, partial cds.				
ACCESSION	AY152072				
VERSION	AY152072.1	GI:28170887			
KEYWORDS	Dengue virus type 4 (DEN-4)				
SEGMENT	1	of 4			
SOURCE	Dengue virus type 4 (DEN-4)				
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.				
REFERENCE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)				
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
TITLE	Selection-Driven Evolution of Emergent Dengue Virus				
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)				
PUBMED	12832629				
REFERENCE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
TITLE	Selection-Driven Evolution of Emergent Dengue Virus				
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)				
PUBMED	12832629				
REFERENCE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
TITLE	Selection-Driven Evolution of Emergent Dengue Virus				
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)				
PUBMED	12832629				
REFERENCE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
TITLE	Selection-Driven Evolution of Emergent Dengue Virus				
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)				
PUBMED	12832629				
REFERENCE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
TITLE	Selection-Driven Evolution of Emergent Dengue Virus				
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)				
PUBMED	12832629				
REFERENCE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
TITLE	Selection-Driven Evolution of Emergent Dengue Virus				
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)				
PUBMED	12832629				
REFERENCE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
TITLE	Selection-Driven Evolution of Emergent Dengue Virus				
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)				

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VERSION	AY152092.1	VERSION	AY152096.1
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SEGMENT	i of 4	SEGMENT	i of 4
SOURCE	Dengue virus type 4 (DEN-4)	SOURCE	Dengue virus type 4 (DEN-4)
ORGANISM	Dengue virus type 4	ORGANISM	Dengue virus type 4
REFERENCE	1 (bases 1 to 2552)	REFERENCE	1 (bases 1 to 2552)
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.	AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE	Selection-Driven Evolution of Emergent Dengue Virus	TITLE	Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)	JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED	12832629	PUBMED	12832629
FEATURES	2 (bases 1 to 2552)	FEATURES	2 (bases 1 to 2552)
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.	AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE	Direct Submission	TITLE	Direct Submission
JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico	JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
PUBMED	Location/Qualifiers	PUBMED	Location/Qualifiers
FEATURES	1. .2552	FEATURES	1. .2552
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CDS	1. .2552 /note="contains core protein, matrix protein and envelope glycoprotein" /codon_start=1 /product="polyprotein precursor" /protein_id="AAN38375.1" /db_xref="GI:28170930"	CDS	1. .2552 /note="contains core protein, matrix protein and envelope glycoprotein" /codon_start=1 /product="polyprotein precursor" /protein_id="AAN38375.1" /db_xref="GI:28170930"

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Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64
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RESULT 30

AY152100S1

LOCUS

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DEFINITION Dengue virus type 4 D4.112_1995MQ polyprotein precursor, gene,
partial cds.
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ACCESSION

AY152100

VERSION

AY152100.1

GI:28170950

1 of 4

Dengue virus type 4 (DEN-4)

Dengue virus type 4

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

1 (bases 1 to 2552)

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,

Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629

REFERENCE

2 (bases 1 to 2552)

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,

Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Direct Submission

Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio

Piedras, PO Box 23360, San Juan 00931, Puerto Rico

Location/Qualifiers

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Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
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Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64
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RESULT 31

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partial cds.
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ACCESSION

AY152104

VERSION

AY152104.1

GI:28170959

1 of 4

Dengue virus type 4 (DEN-4)

Dengue virus type 4

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

1 (bases 1 to 2552)

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,

Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629

REFERENCE

2 (bases 1 to 2552)

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,

Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Direct Submission

Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio

Piedras, PO Box 23360, San Juan 00931, Puerto Rico

Location/Qualifiers

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RESULT 33
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 DEFINITION
 DENGUE VIRUS TYPE 4 D4.36_1992 POLYPROTEIN PRECURSOR, GENE, PARTIAL CDS.

ACCESSION
 VERSION
 KEYWORDS
 SEGMENT
 SOURCE
 ORGANISM

AY152112
 AY152112.1 GI:28170977
 1 of 4
 DENGUE VIRUS TYPE 4 (DEN-4)
 DENGUE VIRUS TYPE 4
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 AUTHORS

1 (bases 1 to 2552)
 Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
 Selection-Driven Evolution of Emergent Dengue Virus
 Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
 12832629

2 (bases 1 to 2552)
 Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
 Direct Submission
 Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
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RESULT 34
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TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
TITLE
JOURNAL
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
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ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACCGCGAGAGAAACCGCG 64
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RESULT 37
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LOCUS
DEFINITION
Dengue virus type 4 D4.78_1994 polyprotein precursor, gene, partial
cds.
ACCESSION
AY152128
VERSION
AY152128.1
KEYWORDS
SEGMENT
SOURCE
1 of 4
Dengue virus type 4 (DEN-4)
ORGANISM
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
TITLE
JOURNAL
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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JOURNAL
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
source
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/note="acronym: DEN-4"
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KVGRIIISTPLAENTNSVTNIELEPPFGDSYIVIGVNSALTTLHWPFRKSSIGMDFE
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ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACCGCGAGAGAAACCGCG 64
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RESULT 38
AY152132S1
LOCUS
DEFINITION
Dengue virus type 4 D4.77_1994 polyprotein precursor, gene, partial
cds.
ACCESSION
AY152132
VERSION
AY152132.1
KEYWORDS
SEGMENT
SOURCE
1 of 4
Dengue virus type 4 (DEN-4)
ORGANISM
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
TITLE
JOURNAL
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
source
1. .2552
/organism="Dengue virus type 4"
/mol_type="genomic RNA"
/isolate="D4.77_1994"

/db_xref="taxon:11070"
/country="Puerto Rico"
/note="acronym: DEN-4"
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KVGRLVTSPLAENTSNVTNIELEPPFGDSYIVIGVNSALTLHFRKGSISIGKMF
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CDS

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 AATATGCTGAAACGCGAGAGAAACCGCG 64
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RESULT 39
AY152136S1
LOCUS
DEFINITION
Dengue virus type 4 D4.76_1994 polyprotein precursor, gene, partial
cda.
ACCESSION
AY152136
VERSION
AY152136.1 GI:28171031
KEYWORDS
Dengue virus type 4 (DEN-4)
1 of 4
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE
AUTHORS
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
1. .2552
/organism="Dengue virus type 4"
/mol_type="genomic RNA"
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CDS

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
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Db 37 AATATGCTGAAACGCGAGAGAAACCGCG 64
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RESULT 40
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LOCUS
DEFINITION
Dengue virus type 4 D4.82_1994 polyprotein precursor, gene, partial
cda.
ACCESSION
AY152140
VERSION
AY152140.1 GI:28171040
KEYWORDS
Dengue virus type 4 (DEN-4)
1 of 4
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE
AUTHORS
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
1. .2552
/organism="Dengue virus type 4"
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 EVKLPDYGELTDCPRGIDFENMILMKKKKTWLVHKQWFLDLPLPFWTAGADTSEV
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Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

Db 37 AATATGCTGAAACGCGAGAGAAACCGCG 64

RESULT 41

AY152144S1

LOCUS

DEFINITION Dengue virus type 4 D4.83_1994 polyprotein precursor, gene, partial cds.

ACCESSION AY152144

VERSION AY152144.1 GI:28171049

KEYWORDS

SEGMENT

SOURCE

ORGANISM

Dengue virus type 4 (DEN-4)
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

1 (bases 1 to 2552)

REFERENCE

AUTHORS

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,

Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

TITLE

JOURNAL

PUBLISHED

2 (bases 1 to 2552)

REFERENCE

AUTHORS

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,

Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

TITLE

JOURNAL

PUBLISHED

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CDS

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/note="acronym: DEN-4"

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 RAETWMSSEGAKHAQVESWILRNPFGFALLAGFMAYMIGOTGIQRTVFFVLMMLVAP
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 LRTYCEIASINITTATPCPTQGEPLYKEEQQQYICRRDVVDRGWGNGCGLFGKGGV
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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

Db 37 AATATGCTGAAACGCGAGAGAAACCGCG 64

RESULT 42

AY152148S1

LOCUS

DEFINITION Dengue virus type 4 D4.81_1994 polyprotein precursor, gene, partial cds.

ACCESSION AY152148

VERSION AY152148.1 GI:28171058

KEYWORDS

SEGMENT

SOURCE

ORGANISM

Dengue virus type 4 (DEN-4)

1 of 4

Dengue virus type 4

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

1 (bases 1 to 2552)

REFERENCE

AUTHORS

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,

Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

TITLE

JOURNAL

Submitted (18-SEP-2002)

Location/Qualifiers

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/organism="Dengue virus type 4"

/mol_type="genomic RNA"

/isolate="D4.81_1994"

/db_xref="taxon:11070"

/country="Puerto Rico"

/note="acronym: DEN-4"

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STYRKAKMILGETAMDFGSGVGLFTSLGKAVHQVFGSVVITTFMGVSWMRILIGF

LVLMIGTNSRNTSMAMTCAVGGITLFLGFTVQADMCGCVSWSGRELKCGSGIFVVDN

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ORIGIN

Query Match

100.0%; Score 28; DB 14; Length 2552;

Best Local Similarity 100.0%; Pred. No. 0.13; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 AATATGCTGAACCGCAGAGAAACCGCG 28
Db	37 AATATGCTGAACCGCAGAGAAACCGCG 64
RESULT 43 AY15215281 LOCUS DEFINITION Dengue virus type 4 D4.87_1994 polypeptide precursor, gene, partial cds.	
ACCESSION	AY15215281
VERSION	AY15215281.1
KEYWORDS	1 of 4
SEGMENT	Dengue virus type 4 (DEN-4)
SOURCE	Dengue virus type 4 (DEN-4)
ORGANISM	Dengue virus type 4 (DEN-4)
REFERENCE	1 (bases 1 to 2552) Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
AUTHORS	1 (bases 1 to 2552) Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
TITLE	1. 2552 /organism="Dengue virus type 4" /mol_type="genomic RNA" /isolate="D4.87.1994" /db_xref="taxon:11070" /country="Puerto Rico" /note="acronym: DEN-4"
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ORIGIN	
Query Match 100.0%; Score 28; DB 14; Length 2552; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 AATATGCTGAACCGCAGAGAAACCGCG 28
Db	37 AATATGCTGAACCGCAGAGAAACCGCG 64
RESULT 45 AY152160S1 LOCUS DEFINITION Dengue virus type 4 D4.37_1992 polypeptide precursor, gene, partial cds.	
ACCESSION	AY152160S1
VERSION	AY152160S1.1
KEYWORDS	1 of 4
SEGMENT	Dengue virus type 4 (DEN-4)
SOURCE	Dengue virus type 4 (DEN-4)
ORGANISM	Dengue virus type 4 (DEN-4)
REFERENCE	1 (bases 1 to 2552) Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
AUTHORS	1 (bases 1 to 2552) Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Db	37 AATATGCTGAACCGCAGAGAAACCGCG 64

AY152160.1 GI:28171085
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submision
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 46
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LOCUS
DEFINITION
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cda.
ACCESSION
AY152164
VERSION
AY152164.1
KEYWORDS
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Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)

REFERENCE
AUTHORS
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submision
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
1..2552
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Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

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LOCUS
DEFINITION
Dengue virus type 4 D4.30_1992 polyprotein precursor, gene, partial
cda.
ACCESSION
AY152168
VERSION
AY152168.1
KEYWORDS
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Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)

AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE	Direct Submission
JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Db	37 AATATGCTGAAACGCGAGAGAAACCGCG 64
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DEFINITION	Dengue virus type 4 D4.27.1992 polyprotein precursor, gene, partial cds.
ACCESSION	AY152172
VERSION	AY152172.1 GI:28171112
KEYWORDS	
SEGMENT	1 of 4
SOURCE	Dengue virus type 4 (DEN-4)
ORGANISM	Dengue virus type 4 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
REFERENCE	1 (bases 1 to 2552)
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE	Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED	12832629
REFERENCE	2 (bases 1 to 2552)
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE	Direct Submission
JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES	Location/Qualifiers
source	1. .2552

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Db 37 AATATGCTGAAACGCGAGAGAAACCGCG 64

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DEFINITION
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ACCESSION
AY152176
VERSION
AY152176.1 GI:28171121
KEYWORDS
1 of 4
SEGMENT
Dengue virus type 4 (DEN-4)
SOURCE
Viruses; SRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE
Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED
12832629
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE
Direct Submission
JOURNAL
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
PUBLISHED
Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 50

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AY152180.1 GI:28171130
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Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
724.058 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatagtctgaacgcgagagaaaccgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

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1: geneseqn1980s:*
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3: geneseqn2000s:*
4: geneseqn2001as:*
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6: geneseqn2002as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	28	100.0	2357	8 ABX13740	Abx13740 Dengue vi
3	28	100.0	2423	12 ADG93319	Adg93319 DEN1 (Pue
4	28	100.0	3381	2 AAT47666	Aat47666 Dengue vi
5	28	100.0	3381	2 AAT47666	Aat47666 Dengue vi
6	28	100.0	3381	12 AAX25114	Aax25114 Dengue vi
7	28	100.0	3381	12 ADQ28715	Adq28715 Dengue vi
8	28	100.0	10616	10 AAD53912	Aad53912 Dengue vi
9	28	100.0	10648	4 AAD14612	Aad14612 Wild-type
10	28	100.0	10648	4 AAD14613	Aad14613 Attenuate
11	28	100.0	10649	10 AAD53911	Aad53911 Recombina
12	28	100.0	10649	10 AAD53910	Aad53910 Dengue vi
13	28	100.0	10717	4 AAD14605	Aad14605 Dengue vi
14	28	100.0	10723	2 AAT49303	Aat49303 cDNA sequ
15	28	100.0	10723	2 AAT49304	Aat49304 cDNA enco
16	28	100.0	10723	4 AAD14614	Aad14614 Dengue vi
17	28	100.0	10723	4 AAD14607	Aad14607 Wild-type
18	28	100.0	10723	4 AAD14606	Aad14606 Dengue vi
19	28	100.0	10723	4 AAD14608	Aad14608 Attenuate
20	28	100.0	10724	12 ADN98025	Adn98025 Dengue vi
21	28	100.0	10756	4 AAD14609	Aad14609 Dengue vi

22	28	100.0	15159	12	ADG93313	Adg93313 DEN2 (Ton
23	26.4	94.3	2426	12	ADG93317	Adg93317 DEN1 (Pue
24	26.4	94.3	10718	2	AAQ51476	Aaq51476 DEN1-S275
25	26.4	94.3	10723	4	AAAD14603	Aad14603 Dengue vi
26	26.4	94.3	10723	4	AAAD14604	Aad14604 Dengue vi
27	26.4	94.3	10735	4	AAAD14602	Aad14602 Attenuate
28	26.4	94.3	10735	4	AAAD14601	Aad14601 Wild-type
29	26.4	94.3	10735	12	ADN98024	Adn98024 Dengue vi
30	26	92.9	26	3	AAC68744	Aac68744 Dengue vi
31	26	92.9	28	2	AAT75917	Aat75917 DEN-2 clo
32	24.8	88.6	10699	4	AAAD14610	Aad14610 Wild-type
33	24.8	88.6	10699	4	AAAD14611	Aad14611 Attenuate
34	24.8	88.6	15153	12	ADG93315	Adg93315 DEN3 (Sle
35	22	78.6	72	6	AAF88836	Aaf88836 Green flu
36	19.2	68.6	1083	3	AAC44997	Aac44997 Arabidops
37	19	67.9	19	12	ADL98061	Adl98061 SCRO gene
38	19	67.9	765	6	ABQ34003	Abq34003 Oligonuc
39	19	67.9	765	6	ABQ34002	Abq34002 Oligonuc
40	19	67.9	28564	10	ADD46068	Add46068 Human gen
41	18.8	67.1	1008	3	AAC46148	Aac46148 Arabidops
42	18.6	66.4	3002	4	ABL229849	Abi229849 Drosophil
43	18.6	66.4	7264	4	ABL229848	Abi229848 Drosophil
44	18.4	65.7	449	3	AAA82355	Aaa82355 N. mening
45	18.4	65.7	1443	3	AAX236361	Aax236361 DNA encod
46	18.4	65.7	1443	9	ABX16417	Abx16417 DNA encod
47	18.4	65.7	1647	12	ADF44354	Adf44354 1647bp se
48	18.4	65.7	4512	2	AAQ22767	Aaq22767 JEV Nakay
49	18.4	65.7	10818	12	ADO07431	Ado07431 Japanese
50	18.4	65.7	10968	12	ADO07437	Ado07437 Japanese

ALIGNMENTS

RESULT 1

ABX15698
ID ABX15698 standard; DNA; 28 BP.

AC ABX15698;

DT 31-MAR-2003 (first entry)

XX Dengue virus detection PCR primer #2.

XX PCR; primer; ss; reverse transcriptase; RT-PCR; dengue fever; DF;
KW dengue haemorrhagic fever; virus; viral detection.

XX Dengue virus.

XX US2002155435-A1.

XX 24-OCT-2002.

XX 28-FEB-2002; 2002US-00085944.

XX 01-MAR-2001; 2001US-0272535P.

XX (WANG/) WANG W.

XX Wang W;

XX WPI; 2003-182625/18.

XX New dengue virus-specific primers, useful for reverse transcriptase-
PT polymerase chain reaction assays, particularly for detecting or
PT quantitating dengue virus in a sample.

XX Claim 28; Page 1; 6pp; English.

XX This invention relates to novel Dengue virus reverse transcriptase (RT)
CC PCR primers which may be used to detect Dengue virus in a sample. Dengue
CC virus is a member of the flavivirus family and causes diseases including
CC dengue fever (DF) and dengue haemorrhagic fever. The invention also

CC comprises a method for detecting and quantitating dengue virus. The
 CC dengue virus-specific primers of the invention are useful in reverse
 CC transcriptase-polymerase chain reaction assays, particularly for
 CC detecting or quantitating dengue virus in a sample. The present sequence
 CC represents a dengue virus specific RT-PCR primer used in the method of
 CC the invention

XX
 SQ Sequence 28 BP; 11 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 8; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 |||||
 Db 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

RESULT 2
 ABX13740
 ID ABX13740 standard; DNA; 2357 BP.
 XX
 AC ABX13740;
 XX
 DT 28-FEB-2003 (first entry)
 XX
 DE Dengue virus type 2 structural gene genome segment.
 XX
 KW Pharmaceutical; ds; immune response; immunogenic; envelope; membrane;
 KW PreM; dengue virus; Den; serotype; flavivirus; Flaviviridae; antigen;
 KW mosquito; Aedes aegyptii; acute undifferentiated fever;
 KW dengue haemorrhagic fever; DHF; dengue shock syndrome; DSS;
 KW immune enhancement phenomenon; DNA vaccine; gene therapy; vaccine;
 KW structural gene; virucide.

XX
 OS Dengue virus.
 XX
 PN US6455509-B1.
 XX
 XX 24-SEP-2002.
 XX
 PF 04-JUN-1997; 97US-00869423.
 XX
 PR 04-JUN-1996; 96US-0017839P.
 XX
 PA (USNA) US SEC OF NAVY.
 XX
 PI Kochel TJ, Porter KR, Raviprakash K, Hoffman SL, Hayes CG;
 XX
 DR WPI; 2003-066244/06.
 XX

XX
 PT New pharmaceutical compositions containing dengue nucleic acids, useful
 PT as a vaccine, particularly for inducing a protective immune response in
 PT mammalian subjects against the dengue virus infection.

XX
 PS Disclosure; Col 17-20; 26pp; English.
 XX
 CC The invention discloses a pharmaceutical composition capable of inducing
 CC an immune response in a mammalian subject, comprising an immunogenic
 CC amount of a eukaryotic plasmid expression vector in pharmaceutical form,
 CC which includes the envelope and membrane (PreM) genes of a dengue type 1,
 CC 2, 3, or 4 virus. Dengue virus (Den) belongs to the flavivirus genus of
 CC the family Flaviviridae and is a positive strand RNA virus encoding ten
 CC proteins. These genes are translated as a polypeptide which is cleaved by
 CC host and viral proteinases. The virus envelope protein is a major antigen
 CC which can be targeted by neutralising antibodies. The membrane protein
 CC also appears on the virion surface and is required for proper processing
 CC of the envelope protein. Dengue viruses are transmitted primarily by the
 CC mosquito, Aedes aegyptii, and can lead to human illnesses ranging from
 CC acute undifferentiated fever to dengue haemorrhagic fever (DHF) and
 CC dengue shock syndrome (DSS). Secondary infections, with a different
 CC serotype, may lead to an immune enhancement phenomenon. The compositions
 CC of the invention are DNA vaccines which are injected into the animal as a

CC technique of gene therapy. The composition is useful as a vaccine,
 CC particularly for inducing a protective immune response in mammalian
 CC subjects against the dengue virus infection. The sequence presented is
 CC the dengue virus type 2 (Den 2) structural gene genome segment

XX
 SQ Sequence 2357 BP; 782 A; 471 C; 595 G; 509 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 8; Length 2357;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 |||||
 Db 60 AATATGCTGAAACGCGAGAGAAACCGCG 87

RESULT 3
 ADG93319
 ID ADG93319 standard; DNA; 2423 BP.
 XX
 AC ADG93319;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE DEN1 (Puerto Rico/94) ME chimeric region DNA SeqID52.
 XX
 KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
 KW dengue type 4; virucide; immunostimulant; vaccine; tetraivalent vaccine;
 KW dengue virus; Delta30; attenuating mutation; humoral response;
 KW cellular response; non-structural protein; structural protein;
 KW dengue virus serotype; gene; ds; plasmid P2.

OS Dengue virus type 1.

XX
 PN WO2003092592-A2.

XX
 PD 13-NOV-2003.

XX
 PF 25-APR-2003; 2003WO-US013279.

XX
 PR 03-MAY-2002; 2002US-0377860P.

XX
 PR 23-DEC-2002; 2002US-0436500P.

XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
 PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
 PI Hanley K;

XX
 DR WPI; 2004-022612/02.

XX
 DR P-PSDB; ADG93320.

XX
 PT New tetraivalent vaccine containing a common nucleotide deletion in the 3'
 PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
 PT of disease in humans caused by dengue virus, or for inducing immune
 PT response.

XX
 PS Disclosure; SEQ ID NO 52; 181pp; English.

XX
 CC This invention relates to a novel immunogenic composition being
 CC tetraivalent and containing a common nucleotide deletion in the 3',
 CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
 CC useful for the development of compounds with a virucide or
 CC immunostimulant activity or as a vaccine. The tetraivalent vaccine is
 CC useful in the prevention of disease in humans caused by dengue virus.
 CC Unlike previous tetraivalent vaccine, the new tetraivalent vaccine is
 CC unique since they contain a common shared attenuating mutation which
 CC eliminates the possibility of generating a virulent wild type virus in a
 CC subject to be vaccinated since each component of the vaccine possesses
 CC the same delta30 attenuating deletion mutation. The vaccine also is able
 CC to induce humoral and cellular responses against all of the (non-
 CC) structural proteins present in each dengue virus serotype. The present
 CC sequence is that of the DEN1 ME chimeric region DNA which is related to
 CC the invention.

XX SQ Sequence 2423 BP; 747 A; 513 C; 636 G; 527 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 12; Length 2423;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 |||||
 Db 138 AATATGCTGAAACGCGAGAGAAACCGCG 165

RESULT 4
 AAT47666
 ID AAT47666 standard; cDNA; 3381 BP.

XX AC AAT47666;

XX 17-OCT-2003 (revised)

DT 19-MAY-1997 (first entry)

XX Dengue virus serotype 2 PR159/S1 mutant sequence.

DE DEN-2; flavivirus; envelope protein; immunisation; vaccine; ss.

XX Dengue virus; serotype 2.

OS Key Location/Qualifiers

FT mutation 1216..1218

FT /*tag= a

FT /note= "codon GAG (Glu) at position 1216-1218 of PR159/S1

FT is GAA (Glu) in wild-type PR159"

FT mutation 1258..1260

FT /*tag= b

FT /note= "codon GTT (Val) at position 1258-1260 of PR159/S1

FT is GTG (Val) in wild-type PR159"

FT mutation 1762..1764

FT /*tag= c

FT /note= "codon GTT (Val) at position 1762-1764 of PR159/S1

FT is ATT (Ile) in wild-type PR159"

FT mutation 1927..1929

FT /*tag= d

FT /note= "codon AGC (Ser) at position 1927-1929 of PR159/S1

FT is AGT (Ser) in wild-type PR159"

XX WO9637221-A1.

XX 28-NOV-1996.

XX 24-MAY-1996; 96WO-US007627.

XX 24-MAY-1995; 95US-00448734.

PR 07-JUN-1995; 95US-00488807.

PR 10-JUL-1995; 95US-00500469.

XX (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.

XX Ivy JM, Nakano E, Clements D;

XX WPI; 1997-020938/02.

DR P-PSDB; AAW09409.

XX Subunit vaccine against flavivirus infection - contg. recombinant

PT envelope protein in secretable form, used for immunising against

PT flavivirus infection.

XX Example 1; Fig 3A-D; 121pp; English.

XX A cDNA sequence of dengue virus serotype 2 (DEN-2) mutant strain PR159/S1

CC shows 4 differences from the wild-type DEN-2 PR159. This results in a

CC conservative mutation in domain B of S1 that may be involved in the

CC attenuation of this small-plaque, temp.-sensitive variant. The cDNA

CC encodes the capsid, pre-membrane, envelope and NS1 proteins (AAW09409) of

the virus. The clone can be used to express recombinant secreted

CC polypeptides, comprising portions of the envelope protein (esp. domain B,

CC Gly296-Gly385), in eukaryotic hosts, e.g. yeast (see also AAT47667 and

CC AAT47703-04) and Drosophila, for use in subunit vaccines against viral

CC infection. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 3381;

Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 |||||
 Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 5
 AAX25114
 ID AAX25114 standard; cDNA; 3381 BP.

XX AC AAX25114;

XX 17-OCT-2003 (revised)

DT 05-JUL-1999 (first entry)

XX Dengue virus serotype 2 PR159/S1 viral capsid, pprM, E, NS1 cDNA.

DE Flavivirus; envelope protein; vaccine; infection; diagnosis; ss.

XX Dengue virus; serotype 2.

XX WO9906068-A2.

XX 11-FEB-1999.

XX 27-JUL-1998; 98WO-US015447.

XX 31-JUL-1997; 97US-00904227.

XX (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.

XX Ivy JM, Peters ID, Collier BG, McDonnell M, Harada KE;

XX WPI; 1999-153454/13.

DR P-PSDB; AAY05522.

XX Recombinant dimeric flaviviral envelope vaccine - comprising a dimeric

PT 80%E protein, useful for protecting against flavivirus, especially dengue

PT virus infections.

XX Example 1; Fig 3A-D; 60pp; English.

XX This cDNA sequence encodes the capsid, prM, envelope (E) and NS1 proteins

XX (see AAY05522) of serotype 2 dengue virus DEN-2 strain PR159/S1. This

XX strain served as the source for DEN-2 genes used in the invention. A

XX vaccine for protecting against flavivirus infection comprises a dimeric

XX 80% E protein that has been secreted as a recombinant protein from a

XX eukaryotic cell. 80% E indicates a C-terminally truncated flavivirus E.

XX The dimeric truncated E is formed: (1) by directly linking 2 tandem

XX copies of 80% E via a flexible tether; (2) via the formation of a leucine

XX zipper domain through the homodimeric association of 2 leucine zipper

XX helices each fused to the C-terminus of an 80% E molecule; or (3) via the

XX formation of a non-covalently associated four-helix bundle domain formed

XX upon association of two helix-turn-helix moieties attached to the C-

XX terminus of an 80% E molecule. Dimeric truncated DEN-2 E proteins are

XX efficiently secreted by recombinant cells, are easier to purify than

XX intracellular proteins, and generate a high titer neutralising antibody

XX response. The method is generally applicable to flaviviruses, in

XX particular dengue viruses such as DEN-2, where 80% E comprises amino

XX acids 1-395 of DEN-2 E. The products can also be used for diagnosis of

XX infection. (Updated on 17-OCT-2003 to standardise OS field)

```
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 2; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | | | |
Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 6
ADQ28715
ID ADQ28715 standard; DNA; 3381 BP.
XX
AC ADQ28715;
XX
DT 26-AUG-2004 (first entry)
XX
DE Dengue virus viral capsid, prM, E and NS1 genes.
XX
KW virucide; vaccine; Flavivirus; dimeric 80%E; Drosophila Schneider cell;
immunogenic composition; multivalent immunodiagnostic; dengue virus;
viral capsid; prM gene; E gene; NS1 gene; ds.
XX
OS Dengue virus.
XX
XX Key Location/Qualifiers
FH 1. .3381
FT /*tag= a
FT /product= "Dengue virus viral capsid, prM, E and NS1
FT polyprotein"
XX
XX US749857-B1.
XX
XX 15-JUN-2004.
XX
XX 18-AUG-1999; 99US-00376463.
XX
XX 31-JUL-1997; 97US-00904227.
XX
XX (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
XX
XX Peters ID, Coller BG, McDonnell M, Ivy JM, Harada K;
XX
XX WPI; 2004-438725/41.
XX
XX P-PSDB; ADQ28716.
XX
XX New vaccines for preventing or diagnosing infections caused by dengue
XX virus comprises a therapeutic amount of a dimeric 80%E protein secreted
XX from Drosophila Schneider cells.
XX
XX Example 1; SEQ ID NO 2; 47pp; English.
XX
XX The invention describes a vaccine that generates a protective,
XX neutralising antibody response to a Flavivirus in a murine host. The
XX vaccine comprises a therapeutic amount of a dimeric 80%E, the dimeric
XX 80%E having been secreted as a recombinantly produced protein from
XX Drosophila Schneider cells, and where 80%E represents the N-terminal 80%
XX portion of the protein from residues 1-395. Also described are: an
XX immunogenic polypeptide comprising the dimeric 80%E cited above; an
XX immunogenic composition that generates a protective, neutralising
XX antibody response to a Flavivirus in a murine host, comprising the above
XX immunogenic polypeptide and a physiological carrier; a multivalent
XX immunodiagnostic for the detection of Flavivirus, comprising at least 2
XX of the above immunogenic polypeptides of at least 2 flaviviral serotypes;
XX and an immunodiagnostic kit for the detection of Flavivirus in a test
XX subject, comprising the above immunogenic or multivalent immunodiagnostic
XX polypeptide, a suitable support phase coated with dimeric 80%E, and
XX labeled antibodies immunoreactive to antibodies from the test subject.
XX The composition is useful for preventing or diagnosing infections caused
XX by dengue virus. This sequence encodes Dengue virus gene viral capsid,
XX prM, E and NS1 genes for Dengue virus strain PR159/SI used as the source
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```
CC of DEN-2 genes for the invention.
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 12; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | | | |
Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 7
AADS3912
ID AADS3912 standard; DNA; 10616 BP.
XX
AC AADS3912;
XX
DT 28-MAY-2003 (first entry)
XX
DE Dengue virus type 2 strain rDEN2/4delta30 DNA.
XX
KW Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
OS Dengue virus.
XX
XX Key Location/Qualifiers
FH 97. .10263
FT /*tag= a
FT /product= "DEN4 strain rDEN2/4delta30 protein"
FT mat_peptide
FT /*tag= c
FT /product= "Anchored capsid protein"
FT mat_peptide
FT /*tag= b
FT /product= "Virion capsid protein"
FT mat_peptide
FT /*tag= d
FT /product= "Membrane precursor protein"
FT mat_peptide
FT /*tag= e
FT /product= "Membrane protein"
FT mat_peptide
FT /*tag= f
FT /product= "Envelope protein"
FT mat_peptide
FT /*tag= g
FT /product= "NS1 protein"
FT mat_peptide
FT /*tag= h
FT /product= "NS2A protein"
FT mat_peptide
FT /*tag= i
FT /product= "NS2B protein"
FT mat_peptide
FT /*tag= j
FT /product= "NS3 protein"
FT mat_peptide
FT /*tag= k
FT /product= "NS4A protein"
FT mat_peptide
FT /*tag= l
FT /product= "2K protein"
FT mat_peptide
FT /*tag= m
FT /product= "NS4B protein"
FT mat_peptide
FT /*tag= n
FT /product= "NS5 protein"
XX
XX WO200295075-A1.
XX
```

PD 28-NOV-2002.
 XX
 PF 22-MAY-2002; 2002WO-US016308.
 XX
 PR 22-MAY-2001; 2001US-0293049P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (BLAN/) BLANEY J E.
 XX
 PI Whitehead SS, Murphy BR, Hanley KA;
 XX
 DR WPI; 2003-120809/11.
 DR P-PSDB; AAE35314.
 XX
 PT New mutated flavivirus, useful for fine tuning the attenuation and growth
 PT characteristics of dengue virus vaccines for the prevention and/or
 PT treatment of dengue virus infection.
 XX
 PS Disclosure; Page 135-138; 246pp; English.
 XX
 CC The present invention relates to novel mutated flaviviruses comprising a
 CC phenotype in which the viral genome is modified by introduction of a
 CC mutation, singly or in combination, taken from mutations from recombinant
 CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
 CC mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
 CC dengue type 4 virus. The methods and compositions of the invention are
 CC useful for fine tuning the attenuation and growth characteristics of
 CC dengue virus vaccines for the prevention and/or treatment of dengue virus
 CC infection. The present sequence is Dengue virus type 4 strain
 CC rDEN2/4delta30 DNA
 XX
 SQ Sequence 10616 BP; 3365 A; 2219 C; 2743 G; 2289 T; 0 U; 0 Other;

 Query Match 100.0%; Score 28; DB 10; Length 10616;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 DB 136 AATATGCTGAAACGCGAGAGAAACCGCG 163

 RESULT 8
 AAD14612
 ID AAD14612 standard; cDNA; 10648 BP.
 XX
 AC AAD14612;
 XX
 DT 11-SEP-2003 (revised)
 DT 01-NOV-2001 (first entry)
 XX
 DE Wild-type, virulent DEN-4 1036 cDNA.
 XX
 KW Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal;
 KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
 XX
 OS Dengue virus; type IV.
 XX
 Key Location/Qualifiers
 FH 102..10265
 FT /*tag= a
 FT /product= "DEN-4 1036 protein"
 XX
 WO200160847-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 16-FEB-2001; 2001WO-US005142.
 XX
 PR 16-FEB-2000; 2000US-0182829P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX

PI Kinney RM, Kinney CVH, Butrapet S, Gubler DL, Bhamarapravati N;
 DR WPI; 2001-497162/54.
 DR P-PSDB; AAE07991.
 XX
 PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX
 PS Example 3; Page 373-389; 470pp; English.
 XX
 CC The invention relates to avirulent, immunogenic flavivirus chimeras
 CC comprising amino acid mutations in the non-structural proteins of a
 CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
 CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present cDNA
 CC sequence encodes wild-type, virulent dengue-4 (DEN-4) 1036 virus protein
 CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
 CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
 CC contains 5' non-coding region followed by a capsid protein (C) encoding
 CC region, premembrane/membrane protein (prM) encoding region, an envelope
 CC protein (E) encoding region, followed by the region encoding non-
 CC structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
 CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;

 Query Match 100.0%; Score 28; DB 4; Length 10648;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 DB 138 AATATGCTGAAACGCGAGAGAAACCGCG 165

 RESULT 9
 AAD14613
 ID AAD14613 standard; cDNA; 10648 BP.
 XX
 AC AAD14613;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Attenuated, vaccine-strain DEN-4 PDK-48 variant cDNA.
 XX
 KW Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal; mutein;
 KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
 KW ss.
 XX
 OS Dengue virus; type IV.
 XX
 Key Location/Qualifiers
 FH 102..10265
 FT /*tag= a
 FT /product= "DEN-4 PDK-48 protein variant"
 XX
 mutation replace(1211, T)
 FT /*tag= b
 FT mutation replace(1971, G)
 FT /*tag= c
 FT mutation replace(3182, G)
 FT /*tag= d
 FT mutation replace(6660, C)
 FT /*tag= e
 FT mutation replace(6957, A)
 FT /*tag= f

```

FT mutation      replace(7162, T)
FT mutation      /*tag= g
FT mutation      replace(7546, C)
FT mutation      /*tag= h
FT mutation      replace(7623, G)
FT mutation      /*tag= i
XX
PN WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
XX
XX P-PSDB; AAE07992.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX
XX vaccinating against a range of dengue viruses.
XX
XX Example 4; Page 397-413; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX
XX comprising amino acid mutations in the non-structural proteins of a
XX
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX
XX structural genes of the virus are used as a backbone into which the
XX
XX structural protein genes of a second flavivirus strain are inserted.
XX
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX
XX flaviviruses are combined in a pharmaceutical composition to confer
XX
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX
XX to confer simultaneous protection against infections. The present cDNA
XX
XX sequence encodes attenuated dengue-4 (DEN-4) PDK-48 virus protein variant
XX
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX
XX protein (E) encoding region, followed by the region encoding non-
XX
XX structural proteins (NS1-NS2A-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
XX
XX non-coding region. DEN-4 virus passaged in primary dog kidney (PDK) cells
XX
XX 48 times is designated as DEN-4 PDK-48 virus
XX
XX
SQ Sequence 10648 BP; 3294 A; 2214 C; 2807 G; 2333 T; 0 U; 0 Other;
XX
XX Query Match      100.0%; Score 28; DB 4; Length 10648;
XX
XX Best Local Similarity 100.0%; Pred. No. 0.013;
XX
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
Qy 1 AATATGCTGAAACCGAGAGAAACCGCG 28
XX
XX |||||
Db 138 AATATGCTGAAACCGAGAGAAACCGCG 165
XX
XX
RESULT 10
AAD53911
ID AAD53911 standard; DNA; 10649 BP.
XX
XX AC AAD53911;
XX
XX DT 28-MAY-2003 (first entry)
XX
XX Recombinant dengue virus type 4 strain rDEN4 DNA.
XX
XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
XX Dengue virus.

```

```

XX Key      Location/Qualifiers
FH CDS      102..10649
FT          /*tag= a
FT          /product= "DEN4 strain rDEN4 protein"
FT          102..440
FT          /*tag= c
FT          /product= "Anchored capsid protein"
FT          102..398
FT          /*tag= b
FT          /product= "Virion capsid protein"
FT          441..938
FT          /*tag= d
FT          /product= "Membrane precursor protein"
FT          714..938
FT          /*tag= e
FT          /product= "Membrane protein"
FT          939..2423
FT          /*tag= f
FT          /product= "Envelope protein"
FT          2424..3479
FT          /*tag= g
FT          /product= "NS1 protein"
FT          3480..4133
FT          /*tag= h
FT          /product= "NS2A protein"
FT          4134..4523
FT          /*tag= i
FT          /product= "NS2B protein"
FT          4524..6377
FT          /*tag= j
FT          /product= "NS3 protein"
FT          6378..6758
FT          /*tag= k
FT          /product= "NS4A protein"
FT          6638..7562
FT          /*tag= m
FT          /product= "NS4B protein"
FT          6759..6827
FT          /*tag= l
FT          /product= "2K protein"
FT          7563..10262
FT          /*tag= n
FT          /product= "NS5 protein"
XX
XX WO200295075-A1.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-US016308.
XX
XX 22-MAY-2001; 2001US-0293049P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX (BLAN//) BLANEY J E.
XX
XX Whitehead SS, Murphy BR, Hanley KA;
XX
XX WPI; 2003-120809/11.
XX
XX P-PSDB; AAE53313.
XX
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
XX
XX characteristics of dengue virus vaccines for the prevention and/or
XX
XX treatment of dengue virus infection.
XX
XX Disclosure; Page 131-132; 246pp; English.
XX
XX The present invention relates to novel mutated flaviviruses comprising a
XX
XX phenotype in which the viral genome is modified by introduction of a
XX
XX mutation, singly or in combination, taken from mutations from recombinant
XX
XX virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX
XX mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
XX
XX dengue type 4 virus. The methods and compositions of the invention are

```

CC useful for fine tuning the attenuation and growth characteristics of
 CC dengue virus vaccines for the prevention and/or treatment of dengue virus
 CC infection. The present sequence is Dengue virus type 4 strain DEN4 DNA
 XX

SQ Sequence 10649 BP; 3298 A; 2214 C; 2804 G; 2333 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 10; Length 10649;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165

RESULT 11

AAAD53910
 ID AAD53910 standard; DNA; 10649 BP.

XX AC AAD53910;

XX DT 28-MAY-2003 (first entry)

DE Dengue virus type 4 strain 2A DNA.

KW Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.

XX Dengue virus.

FT Key Location/Qualifiers
 FT CDS 102..10649
 FT /product= "DEN4 strain 2A protein"
 FT /tag= a
 FT mat_peptide 102..440
 FT /product= c
 FT /tag= c
 FT mat_peptide 102..398
 FT /product= b
 FT /tag= b
 FT mat_peptide 441..938
 FT /product= d
 FT /tag= d
 FT mat_peptide 714..938
 FT /product= e
 FT /tag= e
 FT mat_peptide 939..2423
 FT /product= f
 FT /tag= f
 FT mat_peptide 2424..3479
 FT /product= g
 FT /tag= g
 FT mat_peptide 3480..4133
 FT /product= h
 FT /tag= h
 FT mat_peptide 4134..4523
 FT /product= i
 FT /tag= i
 FT mat_peptide 4524..6377
 FT /product= j
 FT /tag= j
 FT mat_peptide 6378..6758
 FT /product= k
 FT /tag= k
 FT mat_peptide 6759..6827
 FT /product= l
 FT /tag= l
 FT mat_peptide 6828..7562
 FT /product= m
 FT /tag= m
 FT mat_peptide 7563..10262
 FT /product= n
 FT /tag= n
 FT /product= "NS1 protein"
 FT /product= "NS2A protein"
 FT /product= "NS2B protein"
 FT /product= "NS3 protein"
 FT /product= "NS4A protein"
 FT /product= "NS4B protein"
 FT /product= "NS5 protein"

PN WO200295075-A1.
 PD 28-NOV-2002.
 XX
 XX 22-MAY-2002; 2002WO-US016308.
 XX
 XX 22-MAY-2001; 2001US-0293049P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (BLAN/) BLANEY J E.
 XX
 XX Whitehead SS, Murphy BR, Hanley KA;
 DR WPI; 2003-120809/11.
 DR P-FSDB; AAE35312.

XX New mutated flavivirus, useful for fine tuning the attenuation and growth
 PT characteristics of dengue virus vaccines for the prevention and/or
 PT treatment of dengue virus infection.

XX Disclosure; Page 123-126; 246pp; English.

XX The present invention relates to novel mutated flaviviruses comprising a
 CC phenotype in which the viral genome is modified by introduction of a
 CC mutation, singly or in combination, taken from mutations from recombinant
 CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
 CC mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
 CC dengue type 4 virus. The methods and compositions of the invention are
 CC useful for fine tuning the attenuation and growth characteristics of
 CC dengue virus vaccines for the prevention and/or treatment of dengue virus
 CC infection. The present sequence is Dengue virus type 4 strain 2A DNA

XX SQ Sequence 10649 BP; 3302 A; 2212 C; 2800 G; 2335 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 10; Length 10649;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165

RESULT 12

AAAD14605.

ID AAD14605 standard; cDNA; 10717 BP.

XX AC AAD14605;

XX DT 11-SEP-2003 (revised)

DT 01-NOV-2001 (first entry)

XX Dengue virus (DEN)-2/3-VP1 chimeric cDNA.

KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
 immunogenic; viral disease; pharmaceutical; chimeric; ss.

OS Dengue virus; type II.

OS Dengue virus; type III.

OS Chimeric.

FT Key Location/Qualifiers

FT CDS 97..10266

FT /tag= a

FT /product= "DEN-2/3-VP1 fusion protein"

XX WO200160847-A2.

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005142.

XX 16-FEB-2000; 2000US-0182829P.

```

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PT Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX PI WPI; 2001-497162/54.
XX DR P-PSDB; RAE07984.
XX DR
XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX PT vaccinating against a range of dengue viruses.
XX PS Example 2; Page 203-219; 470pp; English.
XX CC The invention relates to avirulent, immunogenic flavivirus chimeras
XX CC comprising amino acid mutations in the non-structural proteins of a
XX CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX CC structural genes of the virus are used as a backbone into which the
XX CC structural protein genes of a second flavivirus strain are inserted.
XX CC These chimeric viruses elicit pronounced immunogenicity but lack the
XX CC accompanying clinical symptoms of viral disease. Attenuated chimeric
XX CC flaviviruses are combined in a pharmaceutical composition to confer
XX CC simultaneous immunity against several strains of pathogenic flaviviruses
XX CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX CC flavivirus chimeras are also used as immunogens or multivalent vaccines
XX CC to confer simultaneous protection against infections. The present cDNA
XX CC sequence encodes dengue virus (DEN)-2/3-VPI fusion protein related to the
XX CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
XX CC comprising a valine at the non-structural protein (NS3)-250 and the
XX CC premembrane/membrane protein (prM) and an envelope protein (E) from wild-
XX CC type DEN-3 16562 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX SQ Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 4; Length 10717;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
|||:|||||:|||||:|||||:|||||:|||||:
Db 136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 13
AAQ12787
ID AAQ12787 standard; RNA; 10723 BP.
XX AC AAQ12787;
XX DT 25-MAR-2003 (revised)
XX DT 21-NOV-1991 (first entry)
XX DE Dengue 2 virus genome.
XX KW dengue virus; detection; consensus sequence; Flavivirus; PCR; ss.
XX OS Dengue virus.
XX FH Key Location/Qualifiers
XX FT CDS 97..10272
XX FT 712..936
XX FT mat_peptide /product= "M protein"
XX FT 937..2421
XX FT mat_peptide /tag= c
XX FT /product= "E protein"
XX FT 2422..3477
XX FT mat_peptide /tag= d
XX FT /product= "NS1"
XX FT 3478..4131
XX FT mat_peptide /tag= e
XX FT /product= "NS2A"
XX FT 4132..4518

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FT /*tag= f
FT /product= "NS2B"
FT mat_peptide 4519..6375
FT /*tag= g
FT /product= "NS3"
FT mat_peptide 6376..6825
FT /*tag= h
FT /product= "NS4a"
FT mat_peptide 6826..7569
FT /*tag= i
FT /product= "NS4B"
FT mat_peptide 7570..10269
FT /*tag= j
FT /product= "NS5"
XX FR2654113-A.
XX PD 10-MAY-1991.
XX PF 09-NOV-1989; 89FR-00914724.
XX PR 09-NOV-1989; 89FR-00014724.
XX PA (INSP ) INST PASTEUR.
XX PI Vincent D;
XX DR WPI; 1991-225002/31.
XX DR P-PSDB; AAR13166.
XX PT Detection and identification of Flaviviridae in biological sample - by
XX PT amplifying consensus sequence then hybridisation opt. followed by typing,
XX PT e.g. sequencing amplified prod.
XX PS Disclosure; Fig 3; 24pp; French.
XX CC The dengue 2 virus is an example of a member of the Flaviviridae which
XX CC can be identified using the probe pair of the invention. A species-
XX CC specific sequence can be amplified using the claimed oligonucleotides as
XX CC primers in a PCR reaction (see AAQ12788 and AAQ12789). Other viruses
XX CC which can be identified include Japanese encephalitis virus and yellow
XX CC fever virus. (Updated on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 10723 BP; 3557 A; 2251 C; 2647 G; 3 T; 2249 U; 16 Other;

Query Match 100.0%; Score 28; DB 2; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.013;
Matches 25; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
|||:|||||:|||||:|||||:|||||:
Db 136 AAUAGUCGAAACGCGAGAGAAACCGCG 163

RESULT 14
AAT49303
ID AAT49303 standard; cDNA; 10723 BP.
XX AC AAT49303;
XX DT 27-AUG-2003 (revised)
XX DT 11-SEP-1997 (first entry)
XX DE cDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
XX KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
XX KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
XX KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
XX KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
XX KW DHF; DSS; ss.
XX OS Dengue virus type 2 (strain 16681).
XX

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```

FH Key          Location/Qualifiers
FT CDS          97..10272
FT             /*tag= a
FT             /product= "DEN-2 polyprotein
FT             /transl_except(pos:9208..9210,aa:Xaa)"
FT             /note= "Xaa = unknown amino acid"
XX
XX WO9640933-A1.
XX
XX PD 19-DEC-1996.
XX
XX PF 06-JUN-1996; 96WO-US009209.
XX
XX PR 07-JUN-1995; 95US-00483292.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapavati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
XX Kinney R, Trent DW;
XX
XX WPI; 1997-052330/05.
XX P-PSDB; AAW06590.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
XX also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
XX quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 23; Page 107-121; 261pp; English.
XX
XX This sequence encodes the polyprotein from Dengue 2 virus, strain 16681.
XX The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3,
XX NS4A, NS4B and NS5 proteins. A clone of this wildtype viral sequence, PDK
XX -53, may be used in the production of a quadravalent vaccine which
XX provides immunity against all four serotypes of dengue virus. The vaccine
XX also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or
XX a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to
XX protect against infection by all four serotypes of dengue virus, DEN-1,
XX DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue
XX haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used
XX to produce the recombinant protein products of the DNA constructs which
XX are used in the vaccines. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2255 T; 0 U; 2 Other;

Query Match      100.0%; Score 28; DB 2; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAACCGCG 28
    |||||
Db 136 AATATGCTGAAACGCGAGAGAACCGCG 163

RESULT 15
AAT49304
ID AAT49304 standard; cDNA; 10723 BP.
XX
XX AC AAT49304;
XX
XX DT 27-AUG-2003 (revised)
XX DT 12-SEP-1997 (first entry)
XX
XX cDNA encoding polyprotein of attenuated DEN-2 virus, PDK-53.
XX
XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
XX NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
XX Chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
XX dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
XX DHF; DSS; ss.
XX
XX Dengue virus type 2 (strain 16681).
XX Synthetic.

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XX Key          Location/Qualifiers
FT mutation     57
FT             /*tag= b
FT             /note= "C>T mutation"
FT             97..10272
FT             /*tag= a
FT             /product= "DEN-2 attenuated polyprotein
FT             /transl_except(pos:643..645,aa:Xaa)
FT             /transl_except(pos:1135..1137,aa:Xaa)
FT             /transl_except(pos:1393..1395,aa:Xaa)
FT             /transl_except(pos:2809..2811,aa:Xaa)
FT             /transl_except(pos:3040..3042,aa:Xaa)
FT             /transl_except(pos:9208..9210,aa:Xaa)"
FT             /note= "Xaa = unknown amino acid"
FT             524
FT mutation
FT             /*tag= c
FT             /note= "A>T mutation, causes Asp to Val substitution"
FT             2055
FT mutation     2055
FT             /*tag= d
FT             /note= "C>T mutation"
FT             2579
FT mutation     2579
FT             /*tag= e
FT             /note= "G>A mutation, causes Gly to Asp substitution"
FT             4018
FT mutation     4018
FT             /*tag= f
FT             /note= "C>T mutation, causes Leu to Phe substitution"
FT             5547
FT mutation     5547
FT             /*tag= g
FT             /note= "C>T mutation"
FT             6599
FT mutation     6599
FT             /*tag= h
FT             /note= "G>C mutation, causes Gly to Ala substitution"
FT             8571
FT mutation     8571
FT             /*tag= i
FT             /note= "C>T mutation"
XX
XX WO9640933-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US009209.
XX
XX 07-JUN-1995; 95US-00483292.
XX
XX 07-JUN-1995; 95US-00483292.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapavati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
XX Kinney R, Trent DW;
XX
XX WPI; 1997-052330/05.
XX P-PSDB; AAW06591.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
XX also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
XX quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 27; Page 122-136; 261pp; English.
XX
XX This sequence encodes the polyprotein from an attenuated derivative of
XX Dengue 2 virus, strain 16681. The derivative is designated PDK-53. The
XX polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A,
XX NS4B and NS5 proteins. The PDK-53 viral sequence may be used in the
XX production of a quadravalent vaccine which provides immunity against all
XX four serotypes of dengue virus. The vaccine also comprises a chimeric
XX DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus.
XX The new quadravalent vaccines are used to protect against infection by
XX all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which
XX can lead to dengue fever or fatal dengue haemorrhagic fever/dengue shock
XX syndrome (DHF/DSS). Host cells are used to produce the recombinant
XX protein products of the DNA constructs which are used in the vaccines.
XX (Updated on 27-AUG-2003 to correct OS field.)

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```
XX SQ Sequence 10723 BP; 3548 A; 2196 C; 2711 G; 2261 T; 0 U; 7 Other;
Query Match 100.0%; Score 28; DB 2; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | |
Db 136 AATATGCTGAACCGGAGAGAAACCGCG 163

RESULT 16
AAD14614
ID AAD14614 standard; cDNA; 10723 BP.
XX
AC AAD14614;
XX
DT 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Dengue virus (DEN)-2/1-VP1 chimeric cDNA.
XX
KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS Dengue virus; type I.
OS Dengue virus; type II.
OS Chimeric.
XX
Key Location/Qualifiers
FH 97.10272
FT CDS /*tag= a
FT /product= "DEN-2/1-VP1 fusion protein"
XX
WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CVH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
DR P-PSDB; AAE07993.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 5; Page 422-438; 470pp; English.
XX
The invention relates to avirulent, immunogenic flavivirus chimeras
comprising amino acid mutations in the non-structural proteins of a
flavivirus. Chimeric viruses containing the attenuation-mutated non-
structural genes of the virus are used as a backbone into which the
structural protein genes of a second flavivirus strain are inserted.
These chimeric viruses elicit pronounced immunogenicity but lack the
accompanying clinical symptoms of viral disease. Attenuated chimeric
flaviviruses are combined in a pharmaceutical composition to confer
simultaneous immunity against several strains of pathogenic flaviviruses
such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
flavivirus chimeras are also used as immunogens or multivalent vaccines
to confer simultaneous protection against infections. The present cDNA
sequence encodes dengue virus (DEN)-2/1-VP1 fusion protein related to the
invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
comprising a valine at the non-structural protein (NS3)-250 and the
premembrane/membrane protein (prM) and an envelope protein (E) from wild-
type DEN-1 16007 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX

SQ Sequence 10723 BP; 3522 A; 2218 C; 2725 G; 2258 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | |
Db 136 AATATGCTGAACCGGAGAGAAACCGCG 163

RESULT 17
AAD14607
ID AAD14607 standard; cDNA; 10723 BP.
XX
AC AAD14607;
XX
DT 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Wild-type, virulent DEN-2 16681 cDNA.
XX
KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal;
KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
OS Dengue virus; type II.
XX
Key Location/Qualifiers
FH 97.10272
FT CDS /*tag= a
FT /product= "DEN-2 16681 protein"
XX
WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CVH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
DR P-PSDB; AAE07986.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 3; Page 252-268; 470pp; English.
XX
The invention relates to avirulent, immunogenic flavivirus chimeras
comprising amino acid mutations in the non-structural proteins of a
flavivirus. Chimeric viruses containing the attenuation-mutated non-
structural genes of the virus are used as a backbone into which the
structural protein genes of a second flavivirus strain are inserted.
These chimeric viruses elicit pronounced immunogenicity but lack the
accompanying clinical symptoms of viral disease. Attenuated chimeric
flaviviruses are combined in a pharmaceutical composition to confer
simultaneous immunity against several strains of pathogenic flaviviruses
such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
flavivirus chimeras are also used as immunogens or multivalent vaccines
to confer simultaneous protection against infections. The present cDNA
sequence encodes wild-type, virulent dengue-2 (DEN-2) 16681 virus protein
used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
contains 5' non-coding region followed by a capsid protein (C) encoding
region, premembrane/membrane protein (prM) encoding region, an envelope
protein (E) encoding region, followed by the region encoding non-
structural proteins (NS1-NS2A-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
```

```
SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2257 T; 0 U; 0 Other;

Query Match      100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATATGCTGAAACGCGAGAGAAACCGCG 28
      |||||||
DB      136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 19
AADI4606
ID AADI4606 standard; cDNA; 10723 BP.
XX
AC AADI4606;
XX
DT 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Dengue virus (DEN)-2/4-VPI chimeric cDNA.
XX
KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS Dengue virus; type II.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT mutation replace(57, C)
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2/4-VPI fusion protein"
XX
FN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07985.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 3; Page 227-243; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/4-VPI fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC pre-membrane/membrane protein (prM) and an envelope protein (E) from wild-
CC type DEN-4 1036 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;

Query Match      100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATATGCTGAAACGCGAGAGAAACCGCG 28
      |||||||
DB      136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 19
AADI4608
ID AADI4608 standard; cDNA; 10723 BP.
XX
AC AADI4608;
XX
DT 01-NOV-2001 (first entry)
DE Attenuated, vaccine-strain DEN-2 PDK-53 variant cDNA.
XX
KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; muten;
KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
KW ss.
XX
OS Dengue virus; type II.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation replace(57, C)
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2 PDK-53 protein variant"
XX
FN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07987.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 1; Page 276-292; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/4-VPI fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC pre-membrane/membrane protein (prM) and an envelope protein (E) from wild-
CC type DEN-4 1036 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;
```

CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes attenuated dengue-2 (DEN-2) PDK-53 virus protein variant
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region
XX
SQ Sequence 10723 BP; 3552 A; 2198 C; 2711 G; 2262 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 136 AATATGCTGAAACGCGAGAGAAACCGCG 163
RESULT 20
ADN98025
ID ADN98025 standard; DNA; 10724 BP.
XX
AC ADN98025;
XX
DT 29-JUL-2004 (first entry)
XX
DE Dengue Virus isolate New Guinea complete genome sequence.
XX
ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
XX
Dengue virus.
OS
XX
PN WO2004040263-A2.
XX
PD 13-MAY-2004.
XX
PF 31-OCT-2003; 2003WO-US034823.
XX
PR 31-OCT-2002; 2002US-0422755P.
XX
PR 06-JUN-2003; 2003US-0476513P.
XX
XX
PA (HEAL-) HEALTH RES INC.
XX
XX
PI Wong SJ, Pei-Yong S;
XX
XX
XX WPI; 2004-400223/37.
XX
XX
PT New diagnostic kit comprising West Nile Virus (WNV) envelope protein
PT reactive with antibody against WNV and cross-reactive with antibody
PT against a flavivirus, useful in diagnosing flavivirus infection caused by
PT DENV, WNV, JEV or SLEV.
XX
XX
PS Disclosure; Fig 40; 212pp; English.
XX
CC The invention relates to a diagnostic kit comprising at least one
CC isolated and purified polypeptide comprising a West Nile Virus (WNV)
CC envelope (E) protein or its immunogenic fragment having a native
CC conformation or non-denatured structure and that is reactive with
CC antibodies against WNV and cross-reactive with antibodies against a
CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus
CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to

CC the complete nucleotide sequence of the DENV isolate New Guinea.
XX
SQ Sequence 10724 BP; 3542 A; 2212 C; 2725 G; 2245 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 12; Length 10724;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 136 AATATGCTGAAACGCGAGAGAAACCGCG 163
RESULT 21
AAD14609
ID AAD14609 standard; cDNA; 10756 BP.
XX
AC AAD14609;
XX
DT 11-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Dengue virus (DEN)-2/WN-PP1 chimeric cDNA.
XX
KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS Dengue virus; type II.
OS West Nile virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 97..10305
FT /*tag= a
FT /product= "DEN-2/WN-PP1 fusion protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
XX
XX P-PSDB; AAE07988.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 6; Page 300-316; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes dengue virus (DEN)-2/WN-PP1 fusion protein related to
XX the invention. This fusion protein contains DEN-2 16681 backbone and the
XX premembrane/membrane protein (prM) and an envelope protein (E) from West
XX Nile NY99. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-

CC SEP-2003 to standardise OS field)

XX Sequence 10756 BP; 3422 A; 2254 C; 2788 G; 2292 T; 0 U; 0 Other;

SQ Sequence 10756 BP; 3422 A; 2254 C; 2788 G; 2292 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 4; Length 10756;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

DB 136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 22

ADG93313

ID ADG93313 standard; DNA; 15159 BP.

XX AC ADG93313;

XX DT 11-MAR-2004 (first entry)

XX DE DEN2 (Tonga/74) cDNA plasmid P2.

XX KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;

XX KW dengue type 4; virucide; immunostimulant; vaccine; tetraivalent vaccine;

XX KW dengue virus; delta30; attenuating mutation; humoral response;

XX KW cellular response; non-structural protein; structural protein;

XX KW dengue virus serotype; gene; ds; plasmid P2.

XX OS Dengue virus type 2.

XX PN WO2003092592-A2.

XX PD 13-NOV-2003.

XX PF 25-APR-2003; 2003WO-US013279.

XX PR 03-MAY-2002; 2002US-0377860P.

XX PR 23-DEC-2002; 2002US-0436500P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;

XX PI Hanley K;

XX DR WPI; 2004-022612/02.

XX DR P-PSDB; ADG93314.

XX PT New tetraivalent vaccine containing a common nucleotide deletion in the 3'

XX PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing

XX PT of disease in humans caused by dengue virus, or for inducing immune

XX PT response.

XX PS Disclosure; SEQ ID NO 46; 181pp; English.

XX CC This invention relates to a novel immunogenic composition being

XX CC tetraivalent and containing a common nucleotide deletion in the 3'

XX CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be

XX CC useful for the development of compounds with a virucide or

XX CC immunostimulant activity or as a vaccine. The tetraivalent vaccine is

XX CC useful in the prevention of disease in humans caused by dengue virus.

XX CC Unlike previous tetraivalent vaccine, the new tetraivalent vaccine is

XX CC unique since they contain a common shared attenuating mutation which

XX CC eliminates the possibility of generating a virulent wild type virus in a

XX CC subject to be vaccinated since each component of the vaccine possesses

XX CC the same delta30 attenuating deletion mutation. The vaccine also is able

XX CC to induce humoral and cellular responses against all of the (non-

XX CC) structural proteins present in each dengue virus serotype. The present

XX CC sequence is that of the DEN2 cDNA plasmid P2 which is related to the

XX CC invention.

XX SQ Sequence 15159 BP; 4518 A; 3436 C; 3896 G; 3309 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 12; Length 15159;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

DB 136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 23

ADG93317

ID ADG93317 standard; DNA; 2426 BP.

XX AC ADG93317;

XX DT 11-MAR-2004 (first entry)

XX DE DEN1 (Puerto Rico/94) CME chimeric region DNA SeqID50.

XX KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;

XX KW dengue type 4; virucide; immunostimulant; vaccine; tetraivalent vaccine;

XX KW dengue virus; delta30; attenuating mutation; humoral response;

XX KW cellular response; non-structural protein; structural protein;

XX KW dengue virus serotype; gene; ds; plasmid P2.

XX OS Dengue virus type 1.

XX PN WO2003092592-A2.

XX PD 13-NOV-2003.

XX PF 25-APR-2003; 2003WO-US013279.

XX PR 03-MAY-2002; 2002US-0377860P.

XX PR 23-DEC-2002; 2002US-0436500P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;

XX PI Hanley K;

XX DR WPI; 2004-022612/02.

XX DR P-PSDB; ADG93318.

XX PT New tetraivalent vaccine containing a common nucleotide deletion in the 3'

XX PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing

XX PT of disease in humans caused by dengue virus, or for inducing immune

XX PT response.

XX PS Disclosure; SEQ ID NO 50; 181pp; English.

XX CC This invention relates to a novel immunogenic composition being

XX CC tetraivalent and containing a common nucleotide deletion in the 3'

XX CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be

XX CC useful for the development of compounds with a virucide or

XX CC immunostimulant activity or as a vaccine. The tetraivalent vaccine is

XX CC useful in the prevention of disease in humans caused by dengue virus.

XX CC Unlike previous tetraivalent vaccine, the new tetraivalent vaccine is

XX CC unique since they contain a common shared attenuating mutation which

XX CC eliminates the possibility of generating a virulent wild type virus in a

XX CC subject to be vaccinated since each component of the vaccine possesses

XX CC the same delta30 attenuating deletion mutation. The vaccine also is able

XX CC to induce humoral and cellular responses against all of the (non-

XX CC) structural proteins present in each dengue virus serotype. The present

XX CC sequence is that of the DEN1 CME chimeric region DNA which is related to

XX CC the invention.

XX SQ Sequence 2426 BP; 754 A; 509 C; 632 G; 531 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 12; Length 2426;

Best Local Similarity 96.4%; Pred. No. 0.059;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 Db 141 AATATGCTGAACGCGAGAGAAACCGCG 168

RESULT 24
 AAQ51476
 ID AAQ51476 standard; DNA; 10718 BP.
 XX
 AC AAQ51476;
 XX
 AC
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 16-MAY-1994 (first entry)
 XX
 XX DEN1-S275/90 (ECACC V92042111).
 XX
 XX Dengue haemorrhagic fever; DHF; dengue fever; DF; dengue shock syndrome;
 KW DSS; DEN1 polypeptides; ss.
 XX
 XX Dengue virus type 2.
 OS
 XX
 FH Location/Qualifiers
 FT CDS 81..10271
 FT /*tag= a
 FT misc_RNA 81..422
 FT /*tag= b
 FT label= C
 FT misc_RNA 123..422
 FT /*tag= C
 FT label= C'
 FT misc_RNA 423..695
 FT /*tag= d
 FT label= PreM
 FT misc_RNA 696..920
 FT /*tag= e
 FT label= M
 FT misc_RNA 921..2402
 FT /*tag= f
 FT label= E
 FT misc_RNA 2403..3464
 FT /*tag= g
 FT label= NS1
 FT misc_RNA 3465..4112
 FT /*tag= h
 FT label= NS2A
 FT misc_RNA 4113..4499
 FT /*tag= i
 FT label= NS2B
 FT misc_RNA 4500..6359
 FT /*tag= j
 FT label= NS3
 FT misc_RNA 6360..6809
 FT /*tag= k
 FT label= NS4A
 FT misc_RNA 6810..7556
 FT /*tag= l
 FT label= NS4B
 FT misc_RNA 7557..10268
 FT /*tag= m
 FT label= NS5
 XX
 XX WO9322440-A1.
 XX
 XX 11-NOV-1993.
 PD
 XX
 XX 28-APR-1993; 93WO-CA000182.
 PF
 XX 29-APR-1992; 92GB-00009243.
 PR
 XX (UYSI-) UNIV SINGAPORE NAT.
 PA
 XX Tan Y, Fu J, Tan B, Yap E, Chan Y;

XX WPI; 1993-368799/46.
 DR P-PSDB; AAR43662.
 XX
 XX New Dengue virus type 1 strain - used to obtain prods. for detection,
 PT diagnosis, vaccines and treatment involving virus.
 XX
 XX Claim 3; Page 20-34; 55pp; English.
 XX
 CC DEN1 virus, strain S275/90 was isolated from the serum of a dengue
 CC haemorrhagic fever (DHF) patient. RNA was isolated from the virus and
 CC used to prepare cDNA encoding DEN1 polypeptides. Dengue virus type 1
 CC prods. can be used for detection, diagnosis, vaccines (inactivated form)
 CC or treatment of DEN1 infections. The sequences given in AAQ51477-86 are
 CC oligonucleotides used to prepare cDNA fragments corresp. to Dengue virus
 CC proteins, by PCR. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 27-AUG-2003 to correct OS field.)
 XX
 XX Sequence 10718 BP; 3419 A; 2226 C; 2769 G; 2304 T; 0 U; 0 Other;
 SQ
 Query Match 94.3%; Score 26.4; DB 2; Length 10718;
 Best Local Similarity 96.4%; Pred. No. 0.07;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 Db 120 AATATGCTGAACGCGAGAGAAACCGCG 147

RESULT 25
 AAD14603
 ID AAD14603 standard; cDNA; 10723 BP.
 XX
 AC AAD14603;
 XX
 DT 11-SEP-2003 (revised)
 DT 01-NOV-2001 (first entry)
 XX
 XX Dengue virus (DEN) -2/1-VP chimeric cDNA.
 DE
 XX
 KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
 KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
 XX
 OS Dengue virus; type I.
 OS Dengue virus; type II.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 97..10272
 FT /*tag= a
 FT /product= "DEN-2/1-VP fusion protein"
 XX
 XX WO200160847-A2.
 XX
 XX 23-AUG-2001.
 XX
 XX 16-FEB-2001; 2001WO-US005142.
 XX
 XX 16-FEB-2000; 2000US-0182829P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
 XX
 XX WPI; 2001-497162/54.
 DR P-PSDB; AAE07982.
 XX
 XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX
 XX Example 1; Page 155-170; 470pp; English.
 PS
 XX The invention relates to avirulent, immunogenic flavivirus chimeras
 CC

comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DEN)-2/1-VV fusion protein related to the invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone comprising a valine at the non-structural protein (NS3)-250 and the capsid protein (C), premembrane/membrane protein (prM) and an envelope protein (E) from wild-type DEN-1 16007 virus. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 10723 BP; 3514 A; 2229 C; 2722 G; 2258 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 4; Length 10723;
 Best Local Similarity 96.4%; Pred. No. 0.071;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 136 AATATGCTGAACGCGAGAGAAACCGCG 163

RESULT 26
 AAD14604
 ID AAD14604 standard; cDNA; 10723 BP.
 XX
 AC AAD14604;
 XX
 DT 11-SEP-2003 (revised)
 DT 01-NOV-2001 (first entry)
 XX
 DE Dengue virus (DEN)-2/1-VV chimeric cDNA.
 KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
 KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
 OS Dengue virus; type I.
 OS Dengue virus; type II.
 OS Chimeric.
 FH Key Location/Qualifiers
 FT CDS 97..10272
 FT /*tag= a
 FT /product= "DEN-2/1-VV fusion protein"
 XX
 PN WO200160847-A2.
 XX
 PD 23-AUG-2001.
 XX
 XX 16-FEB-2001; 2001WO-US005142.
 XX
 XX 16-FEB-2000; 2000US-0182829P.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Kinney RM, Kinney CVH, Butrapet S, Gubler DL, Bhamarapratvi N;
 FT WPI; 2001-497162/54.
 DR P-PSDB; AAE07983.
 DR
 XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX
 XX Example 1; Page 179-195; 470pp; English.
 PS
 XX The invention relates to avirulent, immunogenic flavivirus chimeras

comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DEN)-2/1-VV fusion protein related to the invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone comprising a valine at the non-structural protein (NS3)-250 and the capsid protein (C), premembrane/membrane protein (prM) and an envelope protein (E) from the vaccine strain of Dengue-1 (DEN-1) PDK-13 virus. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 10723 BP; 3514 A; 2228 C; 2722 G; 2259 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 4; Length 10723;
 Best Local Similarity 96.4%; Pred. No. 0.071;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 136 AATATGCTGAACGCGAGAGAAACCGCG 163

RESULT 27
 AAD14602
 ID AAD14602 standard; cDNA; 10735 BP.
 XX
 AC AAD14602;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Attenuated, vaccine-strain DEN-1 PDK-13 variant cDNA.
 KW Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal; mutein;
 KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
 KW ss.
 OS Dengue virus; type I.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT CDS 95..10273
 FT /*tag= a
 FT /product= "DEN-1 PDK-13 protein variant"
 FT mutation replace(1323, T)
 FT /*tag= b
 FT mutation replace(1541, G)
 FT /*tag= c
 FT mutation replace(1543, A)
 FT /*tag= d
 FT mutation replace(1545, G)
 FT /*tag= e
 FT mutation replace(1567, A)
 FT /*tag= f
 FT mutation replace(1608, C)
 FT /*tag= g
 FT mutation replace(2363, A)
 FT /*tag= h
 FT mutation replace(2695, T)
 FT /*tag= i
 FT mutation replace(2782, C)
 FT /*tag= j
 FT mutation replace(5063, G)
 FT /*tag= k
 FT mutation replace(6048, A)
 FT /*tag= l
 FT mutation replace(6806, A)

```

ET mutation /*tag= m
FT replace(7330, A)
FT /*tag= n
FT replace(9445, C)
FT /*tag= o
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
XX
XX WPI; 2001-497162/54.
XX
XX P-PSDB; AAE07981.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 130-146; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes attenuated dengue-1 (DEN-1) PPK-13 virus protein variant
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX protein (E) encoding region, followed by the region encoding non-
XX structural proteins (NS1-NS2A-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
XX non-coding region
XX
XX Sequence 10735 BP; 3429 A; 2231 C; 2776 G; 2299 T; 0 U; 0 Other;
XX
XX Query Match 94.3%; Score 26.4; DB 4; Length 10735;
XX Best Local Similarity 96.4%; Pred. No. 0.071;
XX Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
XX |||||
XX 134 AATATGCTGAACCGGAGAGAAACCGCG 161
XX
XX RESULT 28
XX RAD14601
XX ID AAD14601 standard; cDNA; 10735 BP.
XX
XX AC AAD14601;
XX
XX 11-SEP-2003 (revised)
XX DT 01-NOV-2001 (first entry)
XX
XX Wild-type, virulent DEN-1 16007 cDNA.
XX
XX Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal;
XX avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
XX Dengue virus; type I.
XX

```

```

XX Key Location/Qualifiers
XX CDS 95..10273
XX /*tag= a
XX /*product= "DEN-1 16007 protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
XX
XX WPI; 2001-497162/54.
XX
XX P-PSDB; AAE07980.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 106-122; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes wild-type, virulent dengue-1 (DEN-1) 16007 virus protein
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX protein (E) encoding region, followed by the region encoding non-
XX structural proteins (NS1-NS2A-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
XX non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 10735 BP; 3432 A; 2232 C; 2774 G; 2297 T; 0 U; 0 Other;
XX
XX Query Match 94.3%; Score 26.4; DB 4; Length 10735;
XX Best Local Similarity 96.4%; Pred. No. 0.071;
XX Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
XX |||||
XX 134 AATATGCTGAACCGGAGAGAAACCGCG 161
XX
XX Db
XX
XX RESULT 29
XX ADN98024
XX ID ADN98024 standard; DNA; 10735 BP.
XX
XX AC ADN98024;
XX
XX 29-JUL-2004 (first entry)
XX DT
XX
XX Dengue Virus isolate WestPac complete genome sequence.
XX
XX ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
XX Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
XX
XX Dengue virus.
XX

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PN WO2004040263-A2.
XX 13-MAY-2004.
XX
XX 31-OCT-2003; 2003WO-US034823.
XX
XX 31-OCT-2002; 2002US-0422755P.
XX
XX 06-JUN-2003; 2003US-0476513P.
XX
XX (HEAL-) HEALTH RES INC.
XX
XX Wong SJ, Pei-Yong S;
XX
XX WPI; 2004-400223/37.
XX
XX GENBANK; U88535.
XX
XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein
XX reactive with antibody against WNV and cross-reactive with antibody
XX against a flavivirus, useful in diagnosing flavivirus infection caused by
XX DENV, WNV, JEV or SLEV.
XX
XX Disclosure; Fig 39; 212pp; English.
XX
XX The invention relates to a diagnostic kit comprising at least one
XX isolated and purified polypeptide comprising a West Nile Virus (WNV)
XX envelope (E) protein or its immunogenic fragment having a native
XX conformation or non-denatured structure and that is reactive with
XX antibodies against WNV and cross-reactive with antibodies against a
XX flavivirus. The diagnostic kit is useful in diagnosing flavivirus
XX infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
XX the complete nucleotide sequence of the DENV isolate WestPac.
XX
XX Sequence 10735 BP; 3421 A; 2245 C; 2774 G; 2295 T; 0 U; 0 Other;
XX
XX Query Match 94.3%; Score 26.4; DB 12; Length 10735;
XX Best Local Similarity 96.4%; Pred. No. 0.071;
XX Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGG 28
   |||||
Db 134 AATATGCTGAACGCGAGAGAAACCGG 161

RESULT 30
AAC68744
ID AAC68744 standard; DNA; 26 BP.
AC AAC68744;
XX
XX 23-FEB-2001 (first entry)
DT
XX
XX Dengue virus type 2 upper primer.
DE
XX
XX Dengue virus; antiinflammatory; haemostatic; antibacterial; sepsis;
XX immunosuppressive; immunomodulator; cardiant; cytostatic; cachexia;
XX neuroprotective; respiratory; inflammation; infection; Crohn's disease;
XX multiple sclerosis; autoimmune disorder; cardiovascular disorder;
XX chronic myelogenous leukaemia; inflammatory bowel disease; PCR primer;
XX ss.
XX
XX Dengue virus.
OS
XX
XX WO200064479-A1.
PN
XX
XX 02-NOV-2000.
PD
XX
XX 26-APR-2000; 2000WO-US011700.
PF
XX
XX 27-APR-1999; 99US-00301274.
PR
XX
XX (ANTI-) ANTIBODY SYSTEMS INC.
PA
XX
XX Fredeking TM, Ignatyev GM;
PI

```

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XX WPI; 2000-679646/66.
XX
XX Novel compositions comprising tetracycline or tetracycline-like compounds
XX for the treatment and/or prevention of acute inflammatory responses and
XX diseases, e.g. septic shock and immune complex-induced colitis.
XX
XX Example 2; Page 103; 183pp; English.
XX
XX The present sequence was used in an invention relating to novel
XX compositions and methods containing tetracycline or tetracycline-like
XX compounds for treating and/or preventing acute inflammatory responses and
XX diseases. Such diseases include acute inflammatory conditions associated
XX with viral haemorrhagic diseases (including diseases caused by
XX Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses);
XX parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
XX disorders, acute cardiovascular events, chronic myelogenous leukaemia and
XX transplanted bone marrow-induced graft-versus-host disease, septic shock,
XX immune complex-induced colitis, cerebrospinal fluid inflammation,
XX multiple sclerosis, inflammatory responses associated with trauma,
XX systemic inflammatory response syndrome (SIRS), adult respiratory
XX distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
XX and Crohn's disease
XX
XX Sequence 26 BP; 11 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 92.9%; Score 26; DB 3; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 0.051;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCG 26
   |||||
Db 1 AATATGCTGAACGCGAGAGAAACCG 26

RESULT 31
AAT75917
ID AAT75917 standard; DNA; 28 BP.
AC AAT75917;
XX
XX 15-SEP-1997 (first entry)
DT
XX
XX DEN-2 cloning/sequencing sense primer, D2-134.
DE
XX
XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
XX NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
XX chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
XX dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
XX DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.
XX
XX Synthetic.
OS
XX
XX WO9640933-A1.
PN
XX
XX 19-DEC-1996.
PD
XX
XX 06-JUN-1996; 96WO-US009209.
PF
XX
XX 07-JUN-1995; 95US-00483292.
PR
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (UYMA-) UNIV MAHIDOL AT SALAYA.
PA
XX
XX Bhamarapavati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
XX Kinney R, Trent DW;
PI
XX
XX WPI; 1997-052330/05.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
XX also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
XX quadravalent vaccine for protecting against Dengue virus infection.
XX

```

PS Example; Page 100; 261pp; English.

XX The sequences given in AAT75909-T76029 are primers which were used in the

CC amplification, cloning and sequencing of the Dengue-2 viral cDNA's of the

CC invention. The Dengue 2 viral DNA encodes a polyprotein which comprises

CC the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins.

CC The quadravalent vaccine of the invention comprises an attenuated Dengue

CC virus clone, PDK-53, and a chimeric DEN-2/1 virus, a chimeric DEN-2/3

CC virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are

CC used to protect against infection by all four serotypes of dengue virus,

CC DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal

CC dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are

CC used to produce the recombinant protein products of the DNA constructs

CC which are used in the vaccines

XX

SQ Sequence 28 BP; 11 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 92.9%; Score 26; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.051;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCTGAAACGCGAGAGAAACCG 26

DB 3 AATATGCTGAAACGCGAGAGAAACCG 28

|||||

RESULT 32

AAD14610

ID AAD14610 standard; cDNA; 10699 BP.

XX

AC AAD14610;

XX

DT 11-SEP-2003 (revised)

DT 01-NOV-2001 (first entry)

XX

DE Wild-type, virulent DEN-3 16562 cDNA.

XX

XX Flavivirus; Dengue virus-3; DEN-3; vaccine; infection; virucidal;

KW avirulent; immunogenic; viral disease; pharmaceutical; ss.

XX

OS Dengue virus; type III.

XX

XX Key Location/Qualifiers

FT CDS 95..10267

FT /*tag= a

FT /product= "DEN-3 16562 protein"

XX

PN WO200160847-A2.

XX

PD 23-AUG-2001.

XX

PF 16-FEB-2001; 2001WO-US005142.

XX

PR 16-FEB-2000; 2000US-0182829P.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;

XX WPI; 2001-497162/54.

DR P-PSDB; AAE07989.

XX

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for

PT vaccinating against a range of dengue viruses.

XX

XX Example 2; Page 325-341; 470pp; English.

PS

CC The invention relates to avirulent, immunogenic flavivirus chimeras

CC comprising amino acid mutations in the non-structural proteins of a

CC flavivirus. Chimeric viruses containing the attenuation-mutated non-

CC structural genes of the virus are used as a backbone into which the

CC structural protein genes of a second flavivirus strain are inserted.

CC These chimeric viruses elicit pronounced immunogenicity but lack the

CC

CC accompanying clinical symptoms of viral disease. Attenuated chimeric

CC flaviviruses are combined in a pharmaceutical composition to confer

CC simultaneous immunity against several strains of pathogenic flaviviruses

CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic

CC flavivirus chimeras are also used as immunogens or multivalent vaccines

CC to confer simultaneous protection against infections. The present cDNA

CC sequence encodes wild-type, virulent dengue-3 (DEN-3) 16562 virus protein

CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1

CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome

CC contains 5' non-coding region followed by a capsid protein (C) encoding

CC region, premembrane/membrane protein (prM) encoding region, an envelope

CC protein (E) encoding region, followed by the region encoding non-

CC structural proteins (NS1-NS2A-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'

CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 10699 BP; 3437 A; 2224 C; 2779 G; 2259 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 4; Length 10699;

Best Local Similarity 92.9%; Pred. No. 0.37;

Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

DB 134 AATATGCTGAAACGCGAGAGAAACCGTG 161

|||||

RESULT 33

AAD14611

ID AAD14611 standard; cDNA; 10699 BP.

XX

AC AAD14611;

XX

DT 01-NOV-2001 (first entry)

XX

DE Attenuated, vaccine-strain DEN-3 PGMK-30/FRHL-3 variant cDNA.

XX

XX Flavivirus; Dengue virus-3; DEN-3; vaccine; infection; virucidal; mutein;

KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;

XX ss.

XX Dengue virus; type III.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT CDS 95..10267

FT /*tag= a

FT /product= "DEN-3 PGMK-30/FRHL-3 protein variant"

FT mutation replace(550, C)

FT /*tag= b

FT mutation replace(1813, G)

FT /*tag= c

FT mutation replace(1838, A)

FT /*tag= d

FT mutation replace(1913, G)

FT /*tag= e

FT mutation replace(2140, C)

FT /*tag= f

FT mutation replace(3725, T)

FT /*tag= g

FT mutation replace(4781, C)

FT /*tag= h

XX

PN WO200160847-A2.

XX

PD 23-AUG-2001.

XX

PF 16-FEB-2001; 2001WO-US005142.

XX

PR 16-FEB-2000; 2000US-0182829P.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;

```
XX WPI; 2001-497162/54.
DR P-PSDB; AAE07990.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 4; Page 349-365; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present CDNA
XX sequence encodes attenuated dengue-3 (DEN-3) FGMK-30/FRHL-3 (30 passages
XX in primary green monkey kidney (FGMK) cells, followed by 3 passages in
XX foetus rhesus lung cells) virus protein variant used for constructing
XX flavivirus chimeras. Dengue virus types 1-4 (DEN-1 to DEN-4) are mosquito
XX -borne flavivirus pathogens. The flavivirus genome contains 5' non-coding
XX region followed by a capsid protein (C) encoding region,
XX premembrane/membrane protein (prM) encoding region, an envelope protein
XX (E) encoding region, followed by the region encoding non-structural
XX proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3' non-coding
XX region
XX
XX Sequence 10699 BP; 3439 A; 2221 C; 2778 G; 2261 T; 0 U; 0 Other;
XX
XX Query Match 88.6%; Score 24.8; DB 4; Length 10699;
XX Best Local Similarity 92.9%; Pred. No. 0.37;
XX Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
XX |||||
XX 134 AATATGCTGAAACGCGTGAGAAACCGTG 161
XX
XX RESULT 34
XX ADG93315
XX ID ADG93315 standard; DNA; 15153 BP.
XX
XX AC ADG93315;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE DEN3 (Sleman/78) cDNA plasmid P3.
XX
XX immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
XX dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine;
XX dengue virus; delta30; attenuating mutation; humoral response;
XX cellular response; non-structural protein; structural protein;
XX dengue virus serotype; gene; ds; plasmid P3.
XX
XX Dengue virus type 3.
XX
XX WO2003092592-A2.
XX
XX 13-NOV-2003.
XX
XX - 25-APR-2003; 2003WO-US013279.
XX
XX 03-MAY-2002; 2002US-0377860P.
XX
XX 23-DEC-2002; 2002US-0436500P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
XX
XX WPI; 2004-022612/02.
XX P-PSDB; ADG93316.
XX
XX New tetravalent vaccine containing a common nucleotide deletion in the 3'
XX untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
XX of disease in humans caused by dengue virus, or for inducing immune
XX response.
XX
XX Disclosure; SEQ ID NO 48; 181pp; English.
XX
XX This invention relates to a novel immunogenic composition being
XX tetravalent and containing a common nucleotide deletion in the 3'
XX untranslated region of dengue types 1, 2, 3, and 4. The invention may be
XX useful for the development of compounds with a virucide or
XX immunostimulant activity or as a vaccine. The tetravalent vaccine is
XX useful in the prevention of disease in humans caused by dengue virus.
XX Unlike previous tetravalent vaccine, the new tetravalent vaccine is
XX unique since they contain a common shared attenuating mutation which
XX eliminates the possibility of generating a virulent wild type virus in a
XX subject to be vaccinated since each component of the vaccine possesses
XX the same delta30 attenuating deletion mutation. The vaccine also is able
XX to induce humoral and cellular responses against all of the (non-
XX ) structural proteins present in each dengue virus serotype. The present
XX sequence is that of the DEN3 cDNA plasmid P3 which is related to the
XX invention.
XX
XX Sequence 15153 BP; 4434 A; 3440 C; 3943 G; 3336 T; 0 U; 0 Other;
XX
XX Query Match 88.6%; Score 24.8; DB 12; Length 15153;
XX Best Local Similarity 92.9%; Pred. No. 0.39;
XX Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
XX |||||
XX 134 AATATGCTGAAACGCGTGAGAAACCGTG 161
XX
XX RESULT 35
XX AAF88836
XX ID AAF88836 standard; DNA; 72 BP.
XX
XX AC AAF88836;
XX
XX DT 09-JAN-2003 (first entry)
XX
XX DE Green fluorescent protein PCR primer #1.
XX
XX Replicon; structural region; vaccine; subgenomic replicon; gene therapy;
XX structural protein; C protein; PreM protein; E protein; immunisation;
XX GFP; green fluorescent protein; PCR; primer; ss.
XX
XX Unidentified.
XX
XX WO200272803-A2.
XX
XX 19-SEP-2002.
XX
XX 21-FEB-2002; 2002WO-US006962.
XX
XX 09-MAR-2001; 2001US-0274684P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Pang X, Dayton AI, Zhang M;
XX
XX WPI; 2002-723344/78.
XX
XX New subgenomic replicon of dengue virus origin comprising a deletion for
XX the sequence coding for C, PreM and/or E structural proteins, useful as
XX vaccines for immunization against dengue virus infection.
XX
```

PS Example 2; Page 38; 66pp; English.

XX This invention describes a novel subgenomic replicon of dengue virus

CC origin comprising a deletion for the sequence coding for C, PreM and E

CC (DeltaCME), for PreM and E (DeltaME), or for E (DeltaE) structural

CC proteins, and/or which is adapted to receive at least a nucleotide

CC sequence without disrupting its replication capabilities. The products of

CC the invention can be used for constructing (1) a vaccine or a therapeutic

CC comprising the subgenomic replicon and a carrier; (2) a dengue virus-like

CC particle comprising the subgenomic replicon, and structural proteins of

CC the homologous dengue virus, which encapsulates the subgenomic replicon;

CC and (3) methods of immunisation and treatment comprising administering to

CC the individual the subgenomic replicon or the dengue virus like particle

CC cited above. The subgenomic replicons are useful in gene therapy as

CC vaccines for immunisation against dengue virus infection. This sequence

CC represents a PCR primer used with AAF88837 to amplify the green

CC fluorescent protein (GFP) gene cloned into the dengue virus delta-pre-M/E

CC replicon, at the site previously occupied by the pre-M/E genes

XX

SQ Sequence 72 BP; 26 A; 12 C; 24 G; 10 T; 0 U; 0 Other;

Query Match 78.6%; Score 22; DB 6; Length 72;

Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAA 22

Db 28 AATATGCTGAACCGGAGAGAA 49

|||||

RESULT 36

AAC44997/C

ID AAC44997 standard; DNA; 1083 BP.

XX

AC AAC44997;

XX

DT 18-OCT-2000 (first entry)

XX

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 44912.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway; metabolic pathway;

KW promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

XX 25-FEB-2000; 2000EP-00301439.

XX

PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127452P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130810P.

PR 28-APR-1999; 99US-0130891P.

PR 30-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 04-MAY-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999; 99US-0137502P.

PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999; 99US-0138847P.

PR 14-JUN-1999; 99US-0139119P.

PR 16-JUN-1999; 99US-0139452P.

PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-0139452P.

PR 18-JUN-1999; 99US-0139454P.

PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999; 99US-0139457P.

PR 18-JUN-1999; 99US-0139458P.

PR 18-JUN-1999; 99US-0139459P.

PR 18-JUN-1999; 99US-0139460P.

PR 18-JUN-1999; 99US-0139461P.

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PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139750P.

PR 18-JUN-1999; 99US-0139763P.

PR 21-JUN-1999; 99US-0139817P.

PR 22-JUN-1999; 99US-0139899P.

PR 23-JUN-1999; 99US-0140353P.

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PR 24-JUN-1999; 99US-0140895P.

PR 28-JUN-1999; 99US-0140823P.

PR 29-JUN-1999; 99US-0140991P.

PR 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-0141842P.

PR 01-JUL-1999; 99US-0142154P.

PR 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.

PR 08-JUL-1999; 99US-0142803P.

PR 09-JUL-1999; 99US-0142920P.

PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.

PR 14-JUL-1999; 99US-0143624P.

PR 15-JUL-1999; 99US-0144005P.

PR 16-JUL-1999; 99US-0144085P.

PR 16-JUL-1999; 99US-0144086P.

PR 19-JUL-1999; 99US-0144325P.

PR 19-JUL-1999; 99US-0144331P.

PR 19-JUL-1999; 99US-0144332P.

PR 19-JUL-1999; 99US-0144333P.

PR 19-JUL-1999; 99US-0144334P.

PR 19-JUL-1999; 99US-0144335P.

PR 20-JUL-1999; 99US-0144352P.

PR 20-JUL-1999; 99US-0144632P.

PR 20-JUL-1999; 99US-0144884P.

PR 21-JUL-1999; 99US-0144814P.

PR 21-JUL-1999; 99US-0145086P.

PR 21-JUL-1999; 99US-0145088P.

PR 21-JUL-1999; 99US-0145089P.

PR 22-JUL-1999; 99US-0145087P.

PR 22-JUL-1999; 99US-0145089P.

PR 22-JUL-1999; 99US-0145192P.

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PR 23-JUL-1999; 99US-0145145P.
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PR 23-JUL-1999; 99US-0145224P.
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PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
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PR 02-AUG-1999; 99US-0146388P.
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PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
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PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
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PR 31-AUG-1999; 99US-0151388P.
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PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
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PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
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PR 18-OCT-1999; 99US-0159584P.
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PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.

PR 22-OCT-1999; 99US-0160980P.
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PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 68.6%; Score 19.2; DB 3; Length 1083;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGGCGAGAGAAACC 25
   ||||| ||||| ||||| |||||
Db 34 ATATGCAGAAACGAGAGAGAAAC 11

RESULT 37
ADL98061
ID ADL98061 standard; DNA; 19 BP.
XX
AC ADL98061;
XX
DT 03-JUN-2004 (first entry)
XX
DE SCRO gene specific PCR primer SEQ ID NO:6.
XX
KW strand specific amplification; convertible oligonucleotide;
KW multi-conformational chimeric nucleotide; hemi-nested primer; detection;
KW quantification; identification; drug evaluation;
KW viral replication inhibition; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO2004022784-A2.
XX
PD 18-MAR-2004.
XX
PF 04-SEP-2003; 2003WO-SG000209.
XX
PR 06-SEP-2002; 2002US-0408818P.
XX
PA (UYJO ) JOHNS HOPKINS SINGAPORE PTE LTD.
XX
PI Anwar A, August JT, Too H;
XX
DR WPI; 2004-315577/29.
XX
PT Strand specific amplification, useful in detecting and quantifying
PT nucleic acids, comprises designing a convertible oligonucleotide based on
PT the target nucleic acid strand.
XX
PS Disclosure; SEQ ID NO 6; 79pp; English.
XX
CC The present invention describes a strand specific amplification method
CC which comprises: (a) determining nucleic acid sequences of a target
CC nucleic acid strand; (b) designing a convertible oligonucleotide based,
CC at least in part, on the target nucleic acid strand; (c) conducting a
CC transcription reaction utilising the convertible oligonucleotide and the
CC target nucleic acid strand to proved at least one resultant complementary
CC strand; (d) conducting an amplification reaction to amplify the at least
CC one resultant complementary strand; and (e) analysing the amplification
CC reaction. Also described: (1) a convertible oligonucleotide comprising a
CC first self-annealing portion and a second portion complementary, at least
CC in part, to a target nucleic acid sequence; and (2) designing multi-
CC conformational chimeric nucleotides and hemi-nested primers. The method
CC is useful for strand specific amplification. The method is useful in
```

CC detecting and quantifying nucleic acids, detecting and identifying
CC pathogens and in evaluating drugs that inhibit viral replication. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 67.9%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 TGAACGCGAGAGAAACCG 26
Db 1 TGAACGCGAGAGAAACCG 19
RESULT 38
ABQ34003
ID ABQ34003 standard; DNA; 765 BP.
AC ABQ34003;
XX
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20594.
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention

XX
SQ Sequence 765 BP; 336 A; 230 C; 80 G; 119 T; 0 U; 0 Other;
Query Match 67.9%; Score 19; DB 6; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 ATATGCTGAAACGCGAGAGAAACCGCG 28
Db 441 ATACGCCGAAACGCGAAGAAACGCG 467
RESULT 39
ABQ34002/c
ID ABQ34002 standard; DNA; 765 BP.
XX
AC ABQ34002;
XX
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20593.
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 765 BP; 119 A; 80 C; 230 G; 336 T; 0 U; 0 Other;

```
Query Match      67.9%; Score 19; DB 6; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGCGAGAGAAACCGC 28
   ||| ||||| ||||| |||||
Db 325 ATACGCCGAAACGCGAACGAAACCGC 299

RESULT 40
ADD46068
ID ADD46068 standard; DNA; 28564 BP.
AC ADD46068;
XX
XX
DT 29-JAN-2004 (first entry)
DE Human gene AL138478, SEQ ID NO 11743.
DE Human; ds; gene; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX
XX 01-NOV-2001; 2001US-0346382P.
XX
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEMO ) GEN HOSPITAL CORP.
XX
XX (FARB ) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX
XX GENBANK; AL138478.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction
XX injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
XX therapy). The sequence presented is a human DNA (shown in Table 2 of the
XX specification) which encodes one of the polypeptides of the invention
XX which is differentially expressed during pain. Note: The sequence data
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CC for this patent did not form part of the printed specification, but was
CC obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 28564 BP; 7828 A; 6116 C; 6366 G; 8254 T; 0 U; 0 Other;
Query Match      67.9%; Score 19; DB 10; Length 28564;
Best Local Similarity 81.5%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGC 27
   ||| ||||| ||||| |||||
Db 7881 AAGATGTTGAAAGATGAGAGAAACCGC 7907

RESULT 41
AAC46148/c
ID AAC46148 standard; DNA; 1008 BP.
XX
XX AAC46148;
AC AAC46148;
XX
XX 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 49081.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX
XX 05-MAR-1999; 99US-0123180P.
XX
XX 09-MAR-1999; 99US-0123548P.
XX
XX 23-MAR-1999; 99US-0125788P.
XX
XX 25-MAR-1999; 99US-0126264P.
XX
XX 29-MAR-1999; 99US-0126785P.
XX
XX 01-APR-1999; 99US-0127462P.
XX
XX 06-APR-1999; 99US-0128234P.
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XX 08-APR-1999; 99US-0128714P.
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XX 16-APR-1999; 99US-0129845P.
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XX 19-APR-1999; 99US-0130077P.
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XX 21-APR-1999; 99US-0130449P.
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XX 23-APR-1999; 99US-0130510P.
XX
XX 28-APR-1999; 99US-0130891P.
XX
XX 30-APR-1999; 99US-0131449P.
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XX 30-APR-1999; 99US-0132048P.
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XX 30-APR-1999; 99US-0132407P.
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XX 04-MAY-1999; 99US-0132484P.
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XX 05-MAY-1999; 99US-0132485P.
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XX 06-MAY-1999; 99US-0132486P.
XX
XX 06-MAY-1999; 99US-0132487P.
XX
XX 07-MAY-1999; 99US-0132863P.
XX
XX 11-MAY-1999; 99US-0134256P.
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XX 14-MAY-1999; 99US-0134218P.
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XX 14-MAY-1999; 99US-0134219P.
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XX 14-MAY-1999; 99US-0134221P.
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XX 14-MAY-1999; 99US-0134370P.
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XX 18-MAY-1999; 99US-0134768P.
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XX 19-MAY-1999; 99US-0134941P.
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XX 20-MAY-1999; 99US-0135124P.
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XX 21-MAY-1999; 99US-0135353P.
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XX 24-MAY-1999; 99US-0135629P.
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XX 25-MAY-1999; 99US-0136021P.
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XX 27-MAY-1999; 99US-0136382P.
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XX 28-MAY-1999; 99US-0136782P.
XX
XX 01-JUN-1999; 99US-0137222P.
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PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
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PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
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PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142305P.
PR 06-JUL-1999; 99US-0142309P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144844P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145244P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.

PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149910P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match

67.1%; Score 18.8; DB 3; Length 1008;


```
Best Local Similarity 90.9%; Pred. NO. 1.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGGCAGAGAAACCG 23
DB 71 ATATGCAAGAAACGAGAGAGAA 50

RESULT 42
ABL29849
ID ABL29849 standard; DNA; 3002 BP.
XX AC
XX AB29849;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 41020.
DE Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX Claim 1; SEQ ID NO 41020; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 66.4%; Score 18.6; DB 4; Length 3002;
XX Best Local Similarity 84.0%; Pred. NO. 2e+02;
XX Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGGCAGAGAAACCG 26
DB 253 ATATGCTGAACGGCAGAGAAACCG 277

RESULT 43
ABL29848
ID ABL29848 standard; DNA; 7264 BP.
XX AC
XX AB29848;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 41017.
DE Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX Claim 1; SEQ ID NO 41017; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 66.4%; Score 18.6; DB 4; Length 7264;
XX Best Local Similarity 84.0%; Pred. NO. 2.2e+02;
XX Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 41017.
DE Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX Claim 1; SEQ ID NO 41017; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 66.4%; Score 18.6; DB 4; Length 7264;
XX Best Local Similarity 84.0%; Pred. NO. 2.2e+02;
XX Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGGCAGAGAAACCG 26
DB 1253 ATATGCTGAACGGCAGAGAAACCG 1277

RESULT 44
AAA82355
ID AAA82355 standard; DNA; 449 BP.
XX AC
XX AAA82355;
XX 04-DEC-2000 (first entry)
XX N. meningitidis partial DNA sequence gnm_902 SEQ ID NO:902.
XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
XX antigen; vaccine; diagnosis; infection; antibacterial; identification;
XX Meningococcus B; MenB; ds.
XX Neisseria meningitidis.
XX WO2000022430-A2.
XX 20-APR-2000.
XX 08-OCT-1999; 99WO-US023573.
XX
```

PR 09-OCT-1998; 98US-0103794P.
FR 30-APR-1999; 99US-0132068P.
XX (CHIR) CHIRON CORP.
XX
XX
PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC; Scarlato V;
PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M,
PI Rappuoli R, Pizza M;
XX WPI; 2000-318079/27.
XX
XX Isolated nucleotide sequences of *Neisseria meningitidis* which can be used
PT in the diagnosis and treatment of *N. meningitidis* infection and other
PT *Neisseria* infections, for example, *N. gonorrhoea*.
XX
XX Claim 7; Page 1744; 1760pp; English.
XX
XX The present invention describes methods of obtaining immunogenic proteins
CC from *Neisseria* genomic sequences. AA81453 to AA82414 represent
CC specifically claimed *Neisseria meningitidis* genomic DNA sequences;
CC AA81260 to AA81303 and AA825620 to AA825663 represent *Neisseria* DNA
CC sequences and their corresponding proteins; AA81254 to AA81259 and
CC AA81304 to AA81321 represent PCR primers used in the isolation of
CC *Neisseria meningitidis* DNA sequences; and AA81322 to AA81452 represent
CC *Neisseria meningitidis* MenB polynucleotide ORF sequences, which are all
CC used in the exemplification of the present invention. The nucleic acid
CC sequences, protein sequences, and antibodies against them, can be used in
CC the manufacture of a composition. The composition can be used as a
CC medicament (or in the manufacture of a medicament) for treating,
CC preventing or diagnosing infection due to *Neisseria* bacteria. For
CC example, some of the identified proteins could be components of vaccines
CC against *Meningococcus B*; against all serotypes; and/or against all
CC pathogenic *Neisseriae*. Identification of sequences from the bacterium
CC will also facilitate production of biological probes, particularly
CC organism-specific probes. Attempts to make efficacious *Meningococcus B*
CC vaccines have failed mainly due to antigen tolerance. Multivalent
CC vaccines have also been tried but none have successfully overcome
CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC that may be presumed targets for the immune system and which are not
CC antigenically variable or at least more conserved than other more
CC variable regions
XX
SQ Sequence 449 BP; 105 A; 121 C; 81 G; 142 T; 0 U; 0 Other;

Query Match 65.7%; Score 18.4; DB 3; Length 449;
Best Local Similarity 78.6%; Pred. No. 1.9e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 278 AATATGCTTCAATCGGAGCAAAATCGCG 305

RESULT 45
AAZ36361
ID AAZ36361 standard; DNA; 1443 BP.
XX
AC AAZ36361;
XX
DT 06-AUG-2003 (revised)
DT 22-FEB-2000 (first entry)
XX
XX DNA encoding green pepper fatty acid 13-hydroperoxide lyase (13-HPOL).
XX
KW Guava; fatty acid; 13-hydroperoxide lyase; 13-HPOL; green pepper; banana;
KW 13-hydroperoxide; linoleic acid; alpha-linolenic acid; C6-aldehyde;
KW C12-oxocarboxylic acid; n-hexanal; 3-(Z)-hexen-1-al; 2-(E)-hexen-1-al;
KW alcohol; 13-hydroperoxy-octadeca-9,11-dienoic acid;
KW 13-hydroperoxy-octadeca-9,11,15-trienoic acid; hexan-1-ol;
KW 2-(E)-hexen-1-ol; 3-(Z)-hexen-1-ol; pipol; flavour; fruit flavour;
KW green character; green note; fruit aroma; ss.
XX

OS Capsicum annum.
XX
XX WO9958648-A2.
XX
XX 18-NOV-1999.
XX
XX 05-MAY-1999; 99WO-IB000807.
XX
XX 13-MAY-1998; 98US-00078173.
XX
XX (FIRM) FIRMENICH SA.
XX (UYVA-) UNIV VANDERBILT.
XX (UYZU-) UNIV ZURICH.
XX
XX Whitehead IM, Slusarenko AJ, Waspi U, Gaskin DJH, Brash AR;
XX Tijet N;
XX
XX WPI; 2000-039100/03.
XX
XX Recombinant guava fatty acid 13-hydroperoxide lyase, used in, e.g. fruit
XX flavors.
XX
XX Claim 19; Page 60; 64pp; English.
XX
XX The present sequence encodes a green pepper fatty acid 13-hydroperoxide
CC lyase (13-HPOL). The specification describes guava 13-HPOLs, which
CC contain a unique region (see AAY53763) that is not present in green
CC pepper or banana 13-HPOLs. A recombinant 13-HPOL can be used to cleave a
CC 13-hydroperoxide of linoleic or alpha-linolenic acid into a C6-aldehyde
CC and a C12-oxocarboxylic acid. The 13-HPOL can also be used to prepare n-
CC hexanal, 3-(Z)-hexen-1-al, 2-(E)-hexen-1-al, or their corresponding
CC alcohols from 13-hydroperoxy-octadeca-9,11-dienoic acid or 13-hydroperoxy
CC -octadeca-9,11,15-trienoic acid. N-hexanal, hexan-1-ol, 2-(E)-hexen-1-al,
CC 2-(E)-hexen-1-ol and 3-(Z)-hexen-1-ol (also known as pipol), are used
CC widely in flavours, particularly fruit flavours, to impart a fresh green
CC character. The green notes are also essential for fruit aroma and are
CC used extensively in the aroma industry. note: this sequence appears in
CC the claim but is not specifically claimed, i.e. nucleic acids which
CC hybridize with AA236357, and not with the present sequence are claimed.
CC (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 1443 BP; 418 A; 288 C; 295 G; 442 T; 0 U; 0 Other;

Query Match 65.7%; Score 18.4; DB 3; Length 1443;
Best Local Similarity 78.6%; Pred. No. 2.2e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 933 AAAATGCTGATGCAAGAGAAACTGAG 960

RESULT 46
ABX16417
ID ABX16417 standard; cDNA; 1443 BP.
XX
XX
AC ABX16417;
XX
XX 14-APR-2003 (first entry)
XX
XX DNA encoding green pepper 13-hydroperoxide lyase.
XX
XX Green pepper; 13-hydroperoxide lyase; linoleic acid;
XX alpha-linolenic acid; fatty acid; 13-HPOL; gene; ss.
XX
XX Capsicum annum.
XX
XX Key Location/Qualifiers
XX CDS 1..1443
XX /*tag= a
XX /product= "13-HPOL"
XX /note= "13-hydroperoxide lyase"
XX

PN US2002142407-A1.
 XX 03-OCT-2002.
 PD 09-JAN-2002; 2002US-00042991.
 PF 24-MAY-2000; 2000US-00578533.
 PR (FIRM) FIRMENICH SA.
 XX Whitehead IM, Siusarenko AJ, Waepi U, Gaekin DJH, Brash AR;
 PI Tijet N;
 DR WPI: 2003-197989/19.
 XX P-PSDB; ABG74402.
 DR
 XX
 PT Cleaving 13-hydroperoxide of linoleic acid into aldehyde and
 PT oxocarboxylic acid, and preparing n-hexanal from 13-hydroperoxy-octadeca-
 PT 9,11-dienoic acid, using recombinant fatty acid 13-hydroperoxide lyase.
 XX
 PS Disclosure; Page 21-22; 35pp; English.
 XX
 CC The invention describes a method of cleaving 13-hydroperoxide (I) of
 CC linoleic or alpha-linolenic acid into 6C-aldehyde (A) and 12C-
 CC oxocarboxylic acid (B). The method involves the use of recombinant
 CC protein produced by a vector containing nucleic acid encoding fatty acid
 CC 13-hydroperoxide lyase (HPOU). The method is useful for cleaving 13-
 CC hydroperoxide of linoleic or alpha-linolenic acid into a 6C-aldehyde and
 CC a 12C-oxocarboxylic acid, and for preparing n-hexanal, 3-(Z)-hexen-1-ol,
 CC 2-(E)-hexen-1-ol, 6C-aldehyde, 12C-oxocarboxylic acid, or their
 CC corresponding alcohols from 13-hydroperoxy-octadeca-9,11-dienoic acid or
 CC 13 hydroperoxy-octadeca-9,11,15-trienoic acid. This sequence
 CC encodes green pepper 13-hydroperoxide lyase (13-HPOL)
 XX
 SQ Sequence 1443 BP; 418 A; 288 C; 295 G; 442 T; 0 U; 0 Other;
 Query Match 65.7%; Score 18.4; DB 9; Length 1443;
 Best Local Similarity 78.6%; Pred. No. 2.2e+02;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
 |||||
 DB 933 AAAATGCTGAGATGCAAGAGAACTGAG 960
 |||||
 RESULT 47
 ADF44354
 ID ADF44354 standard; DNA; 1647 BP.
 XX ADF44354;
 AC ADF44354;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE 1647bp sense HPL gene from green pepper.
 XX
 KW transformed; transgenic plant; hydroperoxide lyase; HPL;
 KW volatile biosynthesis HPL enzyme; insect; extermination; isothiocyanate;
 KW agrochemical; gene; green pepper; ds.
 XX
 OS Capsicum annum.
 XX
 PN JP2003339260-A.
 XX
 PD 02-DEC-2003.
 XX
 PF 27-MAY-2002; 2002JP-00153094.
 XX
 PR 27-MAY-2002; 2002JP-00153094.
 XX
 PA (KYOU) UNIV KYOTO.
 XX
 DR WPI; 2004-039487/04.
 XX
 PT A transformed plant in which hydroperoxide lyase gene coding for volatile
 PT biosynthesis hydroperoxide lyase is transduced in sense or antisense
 PT direction, useful in insect-extermination.
 XX
 PS Claim 3; SEQ ID NO 1; 20pp; Japanese.
 XX
 CC The invention relates to a novel transformed plant in which a
 CC hydroperoxide lyase (HPL) gene coding for a volatile biosynthesis HPL
 CC enzyme is transduced in the sense/antisense direction, where activity of
 CC the HPL enzyme is improved or reduced compared to wild-type plant. The
 CC invention further relates an insect-extermination method using the
 CC transformed plant. In the transformed plant, the HPL gene is transduced
 CC in the sense direction and has a fully defined sequence of 1647 base
 CC pairs as given in the specification, and is derived from green pepper.
 CC The HPL gene transduced in the antisense direction has a fully defined
 CC sequence of 1711 base pairs as given in the specification, and is derived
 CC from Arabidopsis thaliana. The biosynthesis of an isothiocyanate compound
 CC is promoted in the transformed plant compared to the wild-type plant. The
 CC transformed plant is a Brassicaceae plant such as A. thaliana. The
 CC transformed plant efficiently exterminates an insect pest and also
 CC effectively inhibits growth of an insect pest. The novel transformed
 CC plant reduces the usage of an agrochemical. This polynucleotide sequence
 CC represents the 1647bp HPL gene from a green pepper of the invention.
 XX
 SQ Sequence 1647 BP; 517 A; 314 C; 320 G; 496 T; 0 U; 0 Other;
 Query Match 65.7%; Score 18.4; DB 12; Length 1647;
 Best Local Similarity 78.6%; Pred. No. 2.3e+02;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
 |||||
 DB 977 AAAATGCTGAGATGCAAGAGAACTGAG 1004
 |||||
 RESULT 48
 AAQ22767
 ID AAQ22767 standard; DNA; 4512 BP.
 XX
 AC AAQ22767;
 XX
 DT 12-AUG-1992 (first entry)
 XX
 DE JEV Nakayama strain prM, E, NS1, NS2A, NS2B and C coding regions.
 XX
 KW Japanese Encephalitis Virus; vaccinia virus donor; plasmid pDr20; ss.
 XX
 OS Japanese encephalitis virus.
 XX
 PN WO9203545-A.
 XX
 PD 05-MAR-1992.
 XX
 PF 05-AUG-1991; 91WO-US005816.
 XX
 PR 15-AUG-1990; 90US-00567960.
 PR 06-JUN-1991; 91US-00711429.
 PR 13-JUN-1991; 91US-00714687.
 PR 17-JUL-1991; 91US-00729800.
 PR 05-AUG-1991; 91WO-UO005816.
 XX
 PA (VIRO-) VIROGENETICS CORP.
 XX
 PI Paoletti E, Pinc, Pinc, Pincus SE;
 XX
 DR WPI; 1992-096889/12.
 XX
 PT Recombinant pox-virus e.g. vaccinia, fowl-pox and canary-pox virus -
 PT contg. DNA from flavi-virus e.g. Japanese encephalitis and yellow fever
 PT virus, used as vaccine.
 XX
 PS Example 9; Fig 17; 117pp; English.
 XX

CC cDNA was prepared from genomic virion RNA obtained from suspension
CC cultures of C6/36 cells infected with a passage 55 suckling mouse brain
CC stock of the Nagayama strain of JEV. EcoRI linkers were ligated to the
CC cDNA fragments for cloning into pBR322. Recombinant plasmids were
CC transformed into E.coli DH5 cells. Plasmid pC20 contained 81 non-coding
CC nucleotides and the coding regions for C and pM. Sequence AAQ22767 is
CC that of the C coding region of pC20, combined with an updated sequence of
CC the pM, E, NS1, NS2A and NS2B coding regions of the Nagayama strain. The
CC sequence begins at the C protein Met initiation codon. A subfragment of
CC pC20 was cloned into pUC18 to give pDr20. This plasmid was then used in
CC the construction of novel recombinants JEV24, JEV27, JEV33 and JEV34.
CC These were transfected into VP410 infected cells to generate vP825,
CC vP829, vP857 and vP864, respectively
XX
SQ Sequence 4512 BP; 1192 A; 1055 C; 1253 G; 1012 T; 0 U; 0 Other;

Query Match 65.7%; Score 18.4; DB 2; Length 4512;
Best Local Similarity 78.6%; Pred. No. 2.5e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 43 AATATGCTGAAACGCGGCTTACCCCGCG 70

RESULT 49
ADO07431
ID ADO07431 standard; DNA; 10818 BP.

AC ADO07431;

DT 15-JUL-2004 (first entry)

DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 9.

XX antiinflammatory; neuroprotective; gene therapy;

KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;

KW Japanese encephalitis.

XX Japanese encephalitis virus.

OS WO2004033690-A1.

PN 22-APR-2004.

PD 09-OCT-2003; 2003WO-KR002081.

PF 09-OCT-2002; 2002KR-00061589.

PR (CIDS-) CID CO LTD.

PA (LEES/) LEE S H.

XX Lee SH, Lee Y, Yun S;

XX WPI; 2004-340933/31.

XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.
FT

PS Example 2; Page 145-152; 265pp; English.

XX The present invention relates to a genomic RNA of the Korean Japanese
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
CC JEV cDNA and reagents are useful in developing vaccines for and in
CC diagnosing and treating Japanese encephalitis. The present sequence is a
CC sequence of the invention.

XX Sequence 10818 BP; 2991 A; 2491 C; 3075 G; 2261 T; 0 U; 0 Other;

Query Match 65.7%; Score 18.4; DB 12; Length 10818;
Best Local Similarity 78.6%; Pred. No. 2.8e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 88 AATATGCTGAAACGCGGCTTACCCCGCG 115

RESULT 50
ADO07437

ID ADO07437 standard; DNA; 10968 BP.

AC ADO07437;

XX 15-JUL-2004 (first entry)

XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 15.

KW antiinflammatory; neuroprotective; gene therapy;

KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;

XX Japanese encephalitis.

OS Japanese encephalitis virus.

XX WO2004033690-A1.

PN 22-APR-2004.

PD 09-OCT-2003; 2003WO-KR002081.

PF 09-OCT-2002; 2002KR-00061589.

PR (CIDS-) CID CO LTD.

PA (LEES/) LEE S H.

XX Lee SH, Lee Y, Yun S;

XX WPI; 2004-340933/31.

XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.
FT

PS Claim 3; Page 154-161; 265pp; English.

XX The present invention relates to a genomic RNA of the Korean Japanese
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
CC JEV cDNA and reagents are useful in developing vaccines for and in
CC diagnosing and treating Japanese encephalitis. The present sequence is a
CC sequence of the invention.

XX Sequence 10968 BP; 3032 A; 2518 C; 3117 G; 2301 T; 0 U; 0 Other;

Query Match 65.7%; Score 18.4; DB 12; Length 10968;
Best Local Similarity 78.6%; Pred. No. 2.8e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 138 AATATGCTGAAACGCGGCTTACCCCGCG 165

Search completed: January 19, 2005, 13:12:16
Job time : 206 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 12:56:22 ; Search time 51 Seconds
(without alignments)
390.237 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatatgctgaacgcgagagaacgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	2357	US-08-869-423-1	Sequence 1, Appli
2	28	100.0	3381	US-08-937-195-1	Sequence 1, Appli
3	28	100.0	3381	US-08-937-195-2	Sequence 2, Appli
4	28	100.0	3381	US-08-915-152-1	Sequence 1, Appli
5	28	100.0	3381	US-08-915-152-2	Sequence 2, Appli
6	28	100.0	3381	US-09-376-463-2	Sequence 1, Appli
7	28	100.0	3381	PCT-US96-07627-1	Sequence 1, Appli
8	28	100.0	3381	PCT-US96-07627-2	Sequence 2, Appli
9	26.4	94.3	10718	US-08-325-436B-1	Sequence 1, Appli
10	18.6	66.4	1145	US-09-270-767-9819	Sequence 9819, Ap
11	18.4	65.7	1443	US-09-078-173A-11	Sequence 11, Appl
12	18.4	65.7	1443	US-10-042-991-11	Sequence 11, Appl
13	18.4	65.7	4512	US-08-224-391-52	Sequence 52, Appl
14	18.4	65.7	4512	US-08-484-304-52	Sequence 52, Appl
15	18.4	65.7	12980	US-08-811-566-5	Sequence 5, Appli
16	18.4	65.7	12980	US-09-034-756-5	Sequence 5, Appli
17	17.6	62.9	3351	US-09-583-110-2433	Sequence 2433, Ap
18	17.4	62.1	763	US-09-270-767-8086	Sequence 8086, Ap
19	17.4	62.1	763	US-09-270-767-23368	Sequence 23368, A
20	17.4	62.1	983	US-08-875-233-11	Sequence 11, Appl
21	17.4	62.1	1227	US-09-328-352-1888	Sequence 1888, Ap
22	17.4	62.1	2646	US-09-221-017B-558	Sequence 558, App
23	17.4	62.1	5026	US-09-549-872B-3	Sequence 3, Appli
24	17.4	62.1	6612	US-09-549-872B-5	Sequence 5, Appli
25	17.4	62.1	11207	US-09-549-872B-2	Sequence 2, Appli
26	17.2	61.4	3243	US-08-611-107-32	Sequence 32, Appl
27	17.2	61.4	24358	US-09-392-812A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-869-423-1
; Sequence 1, Application US/08869423
; Patent No. 6455509
; GENERAL INFORMATION:
; APPLICANT: Kocheil, Tadeusz
; APPLICANT: Porter, Kevin R.
; APPLICANT: Raviprakash, Kanakatte
; APPLICANT: Hoffman, Stephen L.
; APPLICANT: Hayes, Curtis G.
; TITLE OF INVENTION: Dengue Nucleic Acid Vaccines that Induce
; TITLE OF INVENTION: Neutralizing Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Naval Medical Res. & Dev. Cmd.
; STREET: 8901 Wisconsin Ave., Bldg. 1, T-12
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,423
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,839
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kalish, Daniel
; REGISTRATION NUMBER: 33,599
; REFERENCE/DOCKET NUMBER: NC 77,654
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 295-5642
; TELEFAX: (301) 295-1022
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Sequence 1169, Ap
Sequence 1, Appli
Sequence 12, Appl
Sequence 1259, Ap
Sequence 1107, Ap
Sequence 1156, Ap
Sequence 11497, A
Sequence 6977, Ap
Sequence 522, App
Sequence 314, App
Sequence 295, App
Sequence 361, App
Sequence 214, App
Sequence 34, Appl
Sequence 8875, Ap
Sequence 24157, A
Sequence 3544, Ap
Sequence 18826, A
Sequence 105, App
Sequence 1631, Ap
Sequence 16913, A
Sequence 710, App

17 60.7 435 4 US-09-252-991A-1169
17 60.7 1725 4 US-09-623-034-1
17 60.7 2355 3 US-08-913-159-12
17 60.7 2409 4 US-09-252-991A-1259
17 60.7 3378 4 US-09-328-352-4107
16.8 60.0 287 4 US-09-313-294A-1156
16.8 60.0 936 4 US-09-252-991A-11497
16.6 60.0 1746 4 US-09-489-039A-6977
16.6 60.0 1746 4 US-09-313-294A-522
16.6 59.3 702 4 US-08-956-171E-314
16.6 59.3 702 4 US-08-781-986A-314
16.6 59.3 792 4 US-09-134-000C-295
16.6 59.3 851 4 US-08-961-527-361
16.6 59.3 2558 3 US-08-936-165A-214
16.6 59.3 10091 3 US-09-058-489-34
16.6 58.6 424 4 US-09-270-767-8875
16.4 58.6 424 4 US-09-270-767-24157
16.4 58.6 592 4 US-09-270-767-3544
16.4 58.6 592 4 US-09-270-767-18826
16.4 58.6 652 4 US-09-221-017B-105
16.4 58.6 977 4 US-09-270-767-1631
16.4 58.6 977 4 US-09-270-767-16913
16.4 58.6 1404 4 US-09-620-312D-710

MOLECULE TYPE: RNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Dengue virus
 STRAIN: New Guinea C
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: PreM and Envelope
 MAP POSITION: 330-2446
 UNITS: bp
 PUBLICATION INFORMATION:
 AUTHORS: Gruenberg, A
 AUTHORS: Woo, W S
 AUTHORS: Biedrzycka, A
 AUTHORS: Wright, P J
 TITLE: Partial nucleotide sequence and deduced amino
 TITLE: acid sequence of the structural proteins of dengue
 TITLE: virus type 2, New Guinea C and PUO-218 strains
 JOURNAL: J. Gen. Virol.
 VOLUME: 69
 PAGES: 1391-1398
 DATE: 1988
 PUBLICATION INFORMATION:
 AUTHORS: Izrie, K
 AUTHORS: Mohan, P M
 AUTHORS: Sasaguri, Y
 AUTHORS: Putnak, R
 AUTHORS: Padmanabhan, R
 TITLE: Sequence Analysis of Cloned dengue virus type

Patent No. 6455509
 TITLE: 2 Genome (New Guinea-C strain)
 JOURNAL: Gene
 VOLUME: 75
 ISSUE: 2
 PAGES: 197-211
 DATE: 1989
 PUBLICATION INFORMATION:
 AUTHORS: Yaegashi, T
 AUTHORS: Vakharia, V N
 AUTHORS: Page, K
 AUTHORS: Sasaguri, Y
 AUTHORS: Feighny, R
 AUTHORS: Padmanabhan, R
 JOURNAL: Gene
 VOLUME: 46
 ISSUE: 2-3
 PAGES: 257-267
 DATE: 1986

Us-08-869-423-1
 Query Match 100.0%; Score 28; DB 4; Length 2357;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
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 Db 60 AATATGCTGAAACGCGAGAGAAACCGCG 87

RESULT 2
 US-08-937-195-1
 Sequence 1, Application US/08937195
 Patent No. 6136561
 GENERAL INFORMATION:
 APPLICANT: IVY, JOHN M.
 APPLICANT: KAKANO, EILEEN
 APPLICANT: CLEMENTS, DAVID
 TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500

CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,195
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/488,807
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 4733-0003.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3381 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Dengue virus
 STRAIN: Serotype 2 (Den-2)
 IMMEDIATE SOURCE:
 CLONE: Den-2 PRI59/S1
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: group(103, 1940, 1991, 2025)
 OTHER INFORMATION: /note= "Positions in the S1 strain
 OTHER INFORMATION: representing corrections to the wild type DEN-2 PRI59 strain
 OTHER INFORMATION: reported by Hahn(Citation #1)"
 OTHER INFORMATION: /citation= (1)
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1218
 OTHER INFORMATION: /note= "G is replaced by A for
 OTHER INFORMATION: Wild-Type sequence"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1260
 OTHER INFORMATION: /note= "T is replaced by G for
 OTHER INFORMATION: Wild-Type sequence"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1762
 OTHER INFORMATION: /note= "G is replaced by A for
 OTHER INFORMATION: Wild-Type sequence"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1929
 OTHER INFORMATION: /note= "C is replaced by T for
 OTHER INFORMATION: Wild-Type sequence"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 2310
 OTHER INFORMATION: /note= "A is replaced by N for
 OTHER INFORMATION: Wild-Type sequence"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1
 OTHER INFORMATION: /note= "Start of coding strand
 OTHER INFORMATION: sequence for Capsid."

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FEATURE:
NAME/KEY: misc_feature
LOCATION: 343
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for preMembrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Membrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Envelope"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988
US-08-937-195-1

Query Match 100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGGCAGAGAAACCGCG 28
Db 40 AATATGCTGAACGGCAGAGAAACCGCG 67

RESULT 3
US-08-937-195-2
Sequence 2, Application US/08937195
Patent No. 6136561
GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: KAKANO, EILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,195
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,807
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3381
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1216..1218
OTHER INFORMATION: /note= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159/S1"
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1258..1260
OTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159/S1"
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
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NAME/KEY: misc_feature
LOCATION: 1762..1764
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OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159/S1"
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
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NAME/KEY: misc_feature
LOCATION: 1927..1929
OTHER INFORMATION: /note= "AGT(Coding for Ser) is
OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159/S1"
OTHER INFORMATION: strain(citation #1)"
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Capsid"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 343
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for preMembrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Membrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Envelope"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
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; PAGES: 167-180
; DATE: 1988
US-08-937-195-2

Query Match      100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATATGCTGAACGCGAGAGAAACCGCG 28
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DB      40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 4
US-08-915-152-1
; Sequence 1, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hann(Citation #1)"
; OTHER INFORMATION: /citation= ({1})
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1216
; OTHER INFORMATION: /note= "G is replaced by A for

; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1260
; OTHER INFORMATION: /note= "T is replaced by G for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762
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; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1929
; OTHER INFORMATION: /note= "C is replaced by T for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2310
; OTHER INFORMATION: /note= "A is replaced by N for
; OTHER INFORMATION: Wild-Type sequence"
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; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
US-08-915-152-1

Query Match      100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATATGCTGAACGCGAGAGAAACCGCG 28
        |||||||
DB      40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 5
US-08-915-152-2
; Sequence 2, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
```



```

CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,152
FILING DATE: 20-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,469
FILING DATE: 10-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3381
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1216..1218
OTHER INFORMATION: /note= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1258..1260
OTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762..1764
OTHER INFORMATION: /note= "ATT(coding for Ile) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1927..1929
OTHER INFORMATION: /note= "AGT(Coding for Ser) is
OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1

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;
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
;
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
;
; US-08-915-152-2
;
; Query Match 100.0%; Score 28; DB 3; Length 3381;
; Best Local Similarity 100.0%; Pred. No. 0.0012;
; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
; Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67
;
; RESULT 6
; US-09-376-463-2
; Sequence 2, Application US/09376463
; Patent No. 6749857
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
; FILE REFERENCE: 24733-20005.20
; CURRENT APPLICATION NUMBER: US/09/376,463
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
; US-09-376-463-2
;
; Query Match 100.0%; Score 28; DB 4; Length 3381;
; Best Local Similarity 100.0%; Pred. No. 0.0012;
; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

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```
Db
|||||
40 AATATGCTGAAACGCGAGAGAAACCGCG 67

PCT-US96-07627-1
; Sequence 1, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hahn(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1218
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1260
; OTHER INFORMATION: /note= "T is replaced by G for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1929
; OTHER INFORMATION: /note= "C is replaced by T for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2310
; OTHER INFORMATION: /note= "A is replaced by N for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
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```
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
PCT-US96-07627-1
Query Match 100.0%; Score 28; DB 5; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
|||||
Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 8
PCT-US96-07627-2
; Sequence 2, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced for GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: Strain(Citation #1)"
; FEATURE:
```

```
; OTHER INFORMATION: /citation= ({1})
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762..1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ({1})
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(Coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ({1})
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; PCT-US96-07627-2

Query Match 100.0%; Score 28; DB 5; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0012; Mismatches 0; Indels 0; Gaps 0;
Matches 28; Conservative 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | | | |
Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 9
US-08-325-426B-1
; Sequence 1, Application US/08325426B
; Patent No. 6017535
; GENERAL INFORMATION:
; APPLICANT: FU, Jianlin
; APPLICANT: TAN, Boon-Haun
; APPLICANT: YAP, Eu-Hian
; APPLICANT: CHAN, Yow-Cheong
; APPLICANT: TAN, Yin-Hwee
; TITLE OF INVENTION: CDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
; TITLE OF INVENTION: (SINGAPORE STRAIN)
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON and VANDERHYE PC
; STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
```

```
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,426B
; FILING DATE: 16-DEC-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10718 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA sequence corresponding to
; MOLECULE TYPE: the genomic RNA of DEN1-S275/90
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Dengue Fever Virus Type 1
; STRAIN: S275/90
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 81..10268
; US-08-325-426B-1

Query Match 94.3%; Score 26.4; DB 3; Length 10718;
Best Local Similarity 96.4%; Pred. No. 0.0085; Mismatches 1; Indels 0; Gaps 0;
Matches 27; Conservative 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | | | |
Db 120 AATATGCTGAAACGCGAGAGAAACCGCG 147

RESULT 10
US-09-270-767-9819/c
; Sequence 9819, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9819
; LENGTH: 1145
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-9819

Query Match 66.4%; Score 18.6; DB 4; Length 1145;
Best Local Similarity 84.0%; Pred. No. 21; Mismatches 4; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCG 26
| | | | | | | | | | | | | | | | | | | |
Db 452 ATATGCTGAAACGCGAGAGAAACCG 428

RESULT 11
US-09-078-173A-11
; Sequence 11, Application US/09078173A
; Patent No. 6200794
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
```

```
; APPLICANT: Duncan Gaskins
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; FILE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.0001
; CURRENT APPLICATION NUMBER: US/09/078,173A
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-09-078-173A-11

Query Match      65.7%; Score 18.4; DB 3; Length 1443;
Best Local Similarity 78.6%; Pred. No. 28;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
||| ||||| ||| ||||| |||
Db 933 AAAATGCTGAGATGCAAGAGAAACTGAG 960

RESULT 12
US-10-042-991-11
; Sequence 11, Application US/10042991
; Patent No. 6780621
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; FILE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.0001U3
; CURRENT APPLICATION NUMBER: US/10/042,991
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-10-042-991-11

Query Match      65.7%; Score 18.4; DB 4; Length 1443;
Best Local Similarity 78.6%; Pred. No. 28;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
||| ||||| ||| ||||| |||
Db 933 AAAATGCTGAGATGCAAGAGAAACTGAG 960

RESULT 13
US-08-224-391-52
; Sequence 52, Application US/08224391
; Patent No. 5744140
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Pincus, Steven E.
; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
```

```
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,391
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/729,800
; FILING DATE: 17-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4512 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-224-391-52

Query Match      65.7%; Score 18.4; DB 1; Length 4512;
Best Local Similarity 78.6%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
||| ||||| ||| ||||| |||
Db 43 AATATGCTGAACGCGGCTTACCCCGCG 70

RESULT 14
US-08-484-304-52
; Sequence 52, Application US/08484304
; Patent No. 5744141
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Pincus, Steven E.
; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,304
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,391
; FILING DATE:
; APPLICATION NUMBER: US 07/729,800
; FILING DATE: 17-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2340
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 4512 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-484-304-52

Query Match 65.7%; Score 18.4; DB 1; Length 4512;
Best Local Similarity 78.6%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 43 AATATGCTGAACGCGGCTTACCCGCG 70

RESULT 15

US-08-811-566-5/c
Sequence 5, Application US/08811566
Patent No. 6127116
GENERAL INFORMATION:

APPLICANT: Rice, Charles et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESS: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,566

FILING DATE: 03-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1113-1-006

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 12980 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-811-566-5

Query Match 65.7%; Score 18.4; DB 3; Length 12980;
Best Local Similarity 78.6%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 9714 AATATGCTGAACGCGGATACCCGCG 9687

RESULT 16

US-09-034-756-5/c
Sequence 5, Application US/09034756
Patent No. 6392028
GENERAL INFORMATION:
APPLICANT: RICE, CHARLES et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
VIRUS (HCV) AND USES THEREOF

NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,756

FILING DATE: 04-May-1998

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 6029-4831

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-5188

TELEFAX: 314-727-6092

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 12980 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-034-756-5

Query Match 65.7%; Score 18.4; DB 3; Length 12980;
Best Local Similarity 78.6%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 9714 AATATGCTGAACGCGGATACCCGCG 9687

RESULT 17

US-09-583-110-2433
Sequence 2433, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATH00-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 2433

LENGTH: 3351

TYPE: DNA

```
/ ORGANISM: Streptococcus pneumoniae
US-09-583-110-2433

Query Match      62.9%; Score 17.6; DB 4; Length 3351;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAAC 24
    |||||
Db 830 AATATGCTGAAGCTCTTGAGAAAC 853

RESULT 18
US-09-270-767-8086
; Sequence 8086, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8086
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8086

Query Match      62.1%; Score 17.4; DB 4; Length 763;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACGC 27
    |||||
Db 534 AAAATGCGAAAACGCGCAACAAACGC 560

RESULT 19
US-09-270-767-23368
; Sequence 23368, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23368
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23368

Query Match      62.1%; Score 17.4; DB 4; Length 763;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACGC 27
    |||||
Db 534 AAAATGCGAAAACGCGCAACAAACGC 560

RESULT 20
US-08-875-233-11
; Sequence 11, Application US/08875233
; Patent No. 6127601
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell
```

```
/ APPLICANT: Tricoli, David M
/ APPLICANT: Reynolds, John F
/ APPLICANT: Carney, Kim J
/ TITLE OF INVENTION: Plants Resistant to C Strains of
/ TITLE OF INVENTION: Cucumber Mosaic Virus
/ NUMBER OF SEQUENCES: 15
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
/ STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: U.S.A.
/ ZIP: 60689
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/875,233
/ FILING DATE: 26-JUN-1997
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lisa V. Mueller
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-616-5400
/ TELEFAX: 312-616-5460
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 983 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: CUCUMBER MOSAIC VIRUS
/ STRAIN: WHITE LEAF
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..657
/ PUBLICATION INFORMATION:
/ AUTHORS: Quemada, H
/ AUTHORS: Kearney, C
/ AUTHORS: Gonsalves, D
/ AUTHORS: Slightom, J
/ TITLE: Nucleotide Sequences of the Coat Protein
/ TITLE: Genes and Flanking Regions of Cucumber Mosaic
/ JOURNAL: J. Gen. Virol.
/ VOLUME: 70
/ PAGES: 1065-1073
/ DATE: 1989
US-08-875-233-11

Query Match      62.1%; Score 17.4; DB 3; Length 983;
Best Local Similarity 77.8%; Pred. No. 74;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAAACGCG 28
    |||||
Db 113 AGATGCTGAACACTCAATAGAACCTCG 139

RESULT 21
US-09-328-352-1888/c
; Sequence 1888, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
```

FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1888
LENGTH: 1227
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-1888

Query Match 62.1%; Score 17.4; DB 4; Length 1227;
Best Local Similarity 77.8%; Pred. No. 77;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGGAGAGAAACCGC 27
|||||
DB 964 AATATGCAAAACCGGAGAGAAACCGC 938
|||||

RESULT 22
US-09-221-017B-558
Sequence 558, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Montoy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 558:
SEQUENCE CHARACTERISTICS:
LENGTH: 2646 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:

ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...2646
US-09-221-017B-558

Query Match 62.1%; Score 17.4; DB 4; Length 2646;
Best Local Similarity 77.8%; Pred. No. 90;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 AATATGCTGAAACCGGAGAGAAACCGC 28
|||||
DB 1472 ACAGATGAAAGCGGAGAAATCCGCG 1498
|||||

RESULT 23
US-09-549-872B-3
Sequence 3, Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 5026
TYPE: DNA
ORGANISM: Caenorhabditis elegans
US-09-549-872B-3

Query Match 62.1%; Score 17.4; DB 4; Length 5026;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AAACCGCGAGAGAAACCGCG 28
|||||
DB 2034 AAACCGCGAGAGAAACCGCG 2052
|||||

RESULT 24
US-09-549-872B-5
Sequence 5, Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 6612
TYPE: DNA

```

; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/09340
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 08/422,560
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-611-107-32

Query Match 61.4%; Score 17.2; DB 1; Length 3243;
Best Local Similarity 86.4%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TATGCTGAACGCGAGAGAAAC 24
||||| ||| |||||||
DB 926 TATGCTGAACGCGAGAGAAAC 905

RESULT 27
US-09-392-812A-1
; Sequence 1, Application US/09392812A
; Patent No. 653778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Walker, Richard G.
; APPLICANT: Wallingham, Aaron
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 02307E-097600US
; CURRENT APPLICATION NUMBER: US/09/392,812A
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 24358
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: genomic nompC (no-mechanoreceptor potential C)
; OTHER INFORMATION: nucleotide sequence
US-09-392-812A-1

Query Match 61.4%; Score 17.2; DB 4; Length 24358;
Best Local Similarity 86.4%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GCTGAACGCGAGAGAAACCGC 27
||||| ||| |||||||
DB 21468 GCAGAAAGCGAGAGAAACCGC 21489

RESULT 28
US-09-252-991A-1169/c
; Sequence 1169, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1169
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1169

Query Match 60.7%; Score 17; DB 4; Length 435;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ATGCTGAACGCGAGAGAAACCGCG 28
Db 425 AGGTCGAACGCGCGAGAAACCGCG 401

RESULT 29
US-09-623-034-1
; Sequence 1, Application US/09623034
; Patent No. 6765128
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel F.
; APPLICANT: Zhang, Shuqun
; TITLE OF INVENTION: METHODS OF USING A PATHOGEN-ACTIVATABLE
; FILE OF INVENTION: MAP KINASE TO ENHANCE DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: RUT98-0073
; CURRENT APPLICATION NUMBER: US/09/623,034
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US99/03882
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 60/075,685
; PRIOR FILING DATE: 1998-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-623-034-1

Query Match 60.7%; Score 17; DB 4; Length 1725;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACC 25
Db 1231 AATATGCTTAACATAAGAGAAATC 1255

RESULT 30
US-08-913-159-12/c
; Sequence 12, Application US/08913159
; Patent No. 6300109
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Plasmid-derived type II
; TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/913,159
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0179/95
; FILING DATE: 17-FEB-1995
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2355 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Lactococcus lactis subsp. cremoris
; STRAIN: W39
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 744..1283
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /codon_start= 744
; OTHER INFORMATION: /product= "LlaDII restriction endonuclease"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ORF"
; OTHER INFORMATION: /number= 1
; OTHER INFORMATION: /standard_name= "Gene coding for R.LlaDII"
; OTHER INFORMATION: /label= r-llaDII
; OTHER INFORMATION: /note= "The first ten amino acids in this sequence may be
; OTHER INFORMATION: doubtful. However, from base 773 this reading frame gives a
; OTHER INFORMATION: homology with the Bsp6I endonuclease"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1392..2342
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /codon_start= 1392
; OTHER INFORMATION: /product= "LlaDII methylase"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ORF"
; OTHER INFORMATION: /number= 2
; OTHER INFORMATION: /standard_name= "Gene coding for M.LlaDII"
; OTHER INFORMATION: /label= m-llaDII
; OTHER INFORMATION: /note= "The sequence shows 60 % identity and 76 % similarity
; OTHER INFORMATION: with the Bsp6I methylase."
US-08-913-159-12

Query Match 60.7%; Score 17; DB 3; Length 2355;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACC 25
Db 1326 AATATGATGAAAAGCGAGATAAAC 1302

RESULT 31
US-09-252-991A-1259/c
; Sequence 1259, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1259
; LENGTH: 2409
```

```
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1259

Query Match      60.7%; Score 17; DB 4; Length 2409;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 ATGCTGAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | |
Db 2208 AGGTGGAAGCGCGAGAGAAACCGCG 2184

RESULT 32
US-09-328-352-4107
; Sequence 11497, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4107
; LENGTH: 3378
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4107

Query Match      60.7%; Score 17; DB 4; Length 3378;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TATGCTGAACGCGAGAGAAACCGC 27
| | | | | | | | | | | | | | | |
Db 2791 TCTGCTGAACGCGAGAGAAACCGC 2815

RESULT 33
US-09-313-294A-1156
; Sequence 1156, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1156
; LENGTH: 287
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700550474H1
US-09-313-294A-1156

Query Match      60.0%; Score 16.8; DB 4; Length 287;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | |
Db 59 ATTATGCTGAACCTCGAGAGAACTGGG 86

RESULT 34
US-09-252-991A-11497/c
; Sequence 11497, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 11497
; LENGTH: 936
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11497

Query Match      60.0%; Score 16.8; DB 4; Length 936;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | |
Db 901 AAGATGGAGAAACGAGCGGAAACCGCG 874

RESULT 35
US-09-489-039A-6977
; Sequence 6977, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6977
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6977

Query Match      60.0%; Score 16.8; DB 4; Length 1746;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | |
Db 745 AATATGCTGCACGCGGAGAGCCTGCGCG 772

RESULT 36
US-09-313-294A-522/c
; Sequence 522, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
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; SEQ ID NO 522
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549375H1
; LOCATION: 23, 27, 63, 79, 95, 102, 122, 160, 197, 247, 261
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-522

Query Match          59.3%; Score 16.6; DB 4; Length 297;
Best Local Similarity 82.6%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 GCTGAACCGAGAGAAACCGCG 28
DB 55 GCTGAACCGAGAGAGAAACGCG 33

RESULT 37
US-08-956-171E-314
; Sequence 314, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 314:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 314:
US-08-956-171E-314

Query Match          59.3%; Score 16.6; DB 4; Length 702;
Best Local Similarity 82.6%; Pred. No. 1.6e+02;
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Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGAGAGAAA 23
DB 521 AAGATGTTGAAAAACGAGAGAAA 543

RESULT 38
US-08-781-986A-314
; Sequence 314, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 314:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-314

Query Match          59.3%; Score 16.6; DB 4; Length 702;
Best Local Similarity 82.6%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGAGAGAAA 23
DB 521 AAGATGTTGAAAAACGAGAGAAA 543

RESULT 39
US-09-134-000C-295
; Sequence 295, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
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; SEQ ID NO 295
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-295

Query Match      59.3%; Score 16.6; DB 4; Length 792;
Best Local Similarity 82.6%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAA 23
|||||
Db 641 AATATGCGAATAATGCGACAAA 663

RESULT 40
US-08-961-527-361
; Sequence 361, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 361:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 851 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-361

Query Match      59.3%; Score 16.6; DB 4; Length 851;
Best Local Similarity 82.6%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGCGAGAGAAC 24
|||||
Db 682 ACAAGCTAAACGCGACAGAAC 704

RESULT 41
US-08-936-165A-214/c
; Sequence 214, Application US/08936165A
; Patent No. 6348582
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Burnham, Martin
```

```
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Lonetto, Michael
; APPLICANT: Nicholas, Richard
; APPLICANT: Pratt, Julie
; APPLICANT: Reichard, Richard
; APPLICANT: Rosenberg, Martin
; APPLICANT: Ward, Judith
; TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
; TITLE OF INVENTION: Polypeptides and Their Uses
; NUMBER OF SEQUENCES: 534
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,165A
; FILING DATE: 24-SEP-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/027,032
; FILING DATE: 24-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50549
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2558 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-936-165A-214

Query Match      59.3%; Score 16.6; DB 3; Length 2558;
Best Local Similarity 82.6%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAA 23
|||||
Db 2194 AAGATGTTGAAAAACGAGAGAAA 2172

RESULT 42
US-09-058-489-34
; Sequence 34, Application US/09058489
; Patent No. 6103886
; GENERAL INFORMATION:
; APPLICANT: Whitehead Institute for Biomedical Research
; APPLICANT: Lahn, Bruce
; APPLICANT: Page, David
; TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
; FILE REFERENCE: WHI97-08pA
; CURRENT APPLICATION NUMBER: US/09/058,489
; CURRENT FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/041,877
; EARLIER FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 34
; LENGTH: 10091
; TYPE: DNA
; ORGANISM: Human
US-09-058-489-34

Query Match      59.3%; Score 16.6; DB 3; Length 10091;
Best Local Similarity 82.6%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAA 23
Db 2890 AATATGTAGAAAAGCTAGAGAA 2912

RESULT 43
US-09-270-767-8875/c
; Sequence 8875, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8875
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8875

Query Match      58.6%; Score 16.4; DB 4; Length 424;
Best Local Similarity 76.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCG 27
Db 273 ATATGCTGAATGCAGGAGAGCAGC 248

RESULT 44
US-09-270-767-24157/c
; Sequence 24157, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24157
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-24157

Query Match      58.6%; Score 16.4; DB 4; Length 424;
Best Local Similarity 76.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCG 27
Db 273 ATATGCTGAATGCAGGAGAGCAGC 248

RESULT 45
US-09-270-767-3544/c
; Sequence 3544, Application US/09270767
; Patent No. 6703491
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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3544
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-3544

Query Match      58.6%; Score 16.4; DB 4; Length 592;
Best Local Similarity 76.9%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCG 26
Db 436 ATTATGTTGAAACGAGCGGGAACG 411

RESULT 46
US-09-270-767-18826/c
; Sequence 18826, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18826
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-18826

Query Match      58.6%; Score 16.4; DB 4; Length 592;
Best Local Similarity 76.9%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCG 26
Db 436 ATTATGTTGAAACGAGCGGGAACG 411

RESULT 47
US-09-221-017B-105/c
; Sequence 105, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221.017B
; FILING DATE: 23-DEC-1998
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...652
US-09-221-017B-105

Query Match 58.6%; Score 16.4; DB 4; Length 652;
Best Local Similarity 76.9%; Pred. No. 2.e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAAACCGC 27
|||||
Db 480 ATATGCTGAACGCGAGAGAAACCGC 455

RESULT 48

US-09-270-767-1631/c
Sequence 1631, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1631
LENGTH: 977
TYPE: DNA
ORGANISM: *Drosophila melanogaster*
US-09-270-767-1631

Query Match 58.6%; Score 16.4; DB 4; Length 977;
Best Local Similarity 76.9%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAAACCGC 27
|||||
Db 387 ATTTGAGCAACTCGTGTGAACCGC 362

RESULT 49

US-09-270-767-16913/c
Sequence 16913, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 16913
LENGTH: 977
TYPE: DNA
ORGANISM: *Drosophila melanogaster*
US-09-270-767-16913

Query Match 58.6%; Score 16.4; DB 4; Length 977;
Best Local Similarity 76.9%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAAACCGC 27
|||||
Db 387 ATTTGAGCAACTCGTGTGAACCGC 362

RESULT 50

US-09-620-312D-710/c
Sequence 710, Application US/09620312D
Patent No. 6596662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyang
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yuning
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 659662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: Pt_FL_genes Version 1.0
SEQ ID NO 710
LENGTH: 1404
TYPE: DNA
ORGANISM: *Homo sapiens*
FEATURE:
NAME/KEY: CDS
LOCATION: (104)..(916)
US-09-620-312D-710

Query Match 58.6%; Score 16.4; DB 4; Length 1404;
Best Local Similarity 76.9%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCG 26
||| ||| ||| | ||| |||
Db 1245 AATAGGCTAAATGAAAAGAAACCG 1220

Search completed: January 19, 2005, 13:55:03
Job time : 52 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 13:08:52 ; Search time 207 Seconds
(without alignments)
777.222 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatatgtctgaacgcgagagaaacgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:*

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19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	28	100.0	28	13	US-10-085-944-2
2	28	100.0	3381	15	US-10-247-960-2
3	28	100.0	10724	18	US-10-699-550-4
4	26.4	94.3	10735	18	US-10-699-550-3
5	26	92.9	26	9	US-09-840-707A-23
6	26	92.9	26	14	US-10-038-557A-23
7	22	78.6	72	18	US-10-656-721-26
8	19.6	70.0	594	18	US-10-425-115-108018
9	19	67.9	765	18	US-10-363-345A-20593
10	19	67.9	765	18	US-10-363-345A-20594
11	18.8	67.1	1428	15	US-10-369-493-32952
12	18.6	66.4	1602	15	US-10-156-761-2266

c 13	18.6	66.4	9025608	15	US-10-156-761-1	Sequence 1, Appli
c 14	18.4	65.7	1443	13	US-10-042-991-11	Sequence 11, Appli
c 15	18.4	65.7	12305	18	US-10-422-323A-2	Sequence 2, Appli
c 16	18.4	65.7	12315	18	US-10-422-323A-1	Sequence 1, Appli
c 17	18.4	65.7	12980	9	US-09-238-076-5	Sequence 5, Appli
c 18	18.4	65.7	12980	10	US-09-995-937-5	Sequence 5, Appli
c 19	18.4	65.7	12980	10	US-09-917-563-5	Sequence 5, Appli
c 20	18.2	65.0	452	10	US-09-918-995-27460	Sequence 27460, A
c 21	18.2	65.0	2179	9	US-09-823-245A-434	Sequence 434, App
c 22	18.2	65.0	9875	10	US-09-764-891-7878	Sequence 7878, Ap
c 23	17.6	62.9	529	16	US-10-424-599-130933	Sequence 130933,
c 24	17.6	62.9	550	14	US-10-198-846-11819	Sequence 11819, A
c 25	17.6	62.9	838	14	US-10-198-846-3468	Sequence 3468, Ap
c 26	17.6	62.9	945	16	US-10-398-221-2508	Sequence 2508, Ap
c 27	17.6	62.9	945	16	US-10-398-221-2571	Sequence 2571, Ap
c 28	17.6	62.9	966	16	US-10-398-221-553	Sequence 553, App
c 29	17.6	62.9	966	16	US-10-398-221-554	Sequence 554, App
c 30	17.6	62.9	1646	16	US-10-282-122A-29374	Sequence 29374, A
c 31	17.6	62.9	9718	8	US-08-319-974A-1	Sequence 1, Appli
c 32	17.6	62.9	684707	16	US-10-398-221-9	Sequence 9, Appli
c 33	17.6	62.9	684707	16	US-10-398-221-9	Sequence 9, Appli
c 34	17.6	62.9	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
c 35	17.4	62.1	341	17	US-10-767-701-19049	Sequence 19049, A
c 36	17.4	62.1	379	10	US-09-738-269-20	Sequence 20, Appl
c 37	17.4	62.1	379	13	US-10-023-437-20	Sequence 20, Appl
c 38	17.4	62.1	382	17	US-10-437-963-17200	Sequence 17200, A
c 39	17.4	62.1	528	16	US-10-424-599-53946	Sequence 53946, A
c 40	17.4	62.1	558	13	US-10-027-632-237136	Sequence 237136,
c 41	17.4	62.1	558	15	US-10-027-632-237136	Sequence 237136,
c 42	17.4	62.1	589	18	US-10-363-345A-34197	Sequence 34197, A
c 43	17.4	62.1	589	18	US-10-363-345A-34198	Sequence 34198, A
c 44	17.4	62.1	691	18	US-10-363-345A-38631	Sequence 38631, A
c 45	17.4	62.1	691	18	US-10-363-345A-38631	Sequence 38631, A
c 46	17.4	62.1	774	16	US-10-282-122A-39862	Sequence 39862, A
c 47	17.4	62.1	778	16	US-10-282-122A-36749	Sequence 36749, A
c 48	17.4	62.1	983	13	US-10-011-033-11	GENERAL INFORMA
c 49	17.4	62.1	2520	10	US-09-738-269-22	Sequence 22, Appl
c 50	17.4	62.1	2520	13	US-10-023-437-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-10-085-944-2
; Sequence 2, Application US/10085944
; Publication No. US20020155435A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei-Kung
; TITLE OF INVENTION: DETECTION OF DENGUE VIRUS
; FILE REFERENCE: 12563-004001
; CURRENT APPLICATION NUMBER: US/10/085,944
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/272,535
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-085-944-2

Query Match 100.0%; Score 28; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGCAGAGAAACCGCG 28
Db 1 AATATGCTGAACCGCAGAGAAACCGCG 28

```

RESULT 2
US-10-247-960-2
; Sequence 2, Application US/10247960
; Publication No. US20030175304A1
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; FILE REFERENCE: 24733-2005.01
; CURRENT APPLICATION NUMBER: US/10/247,960
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/376,463
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-10-247-960-2

Query Match          100.0%; Score 28; DB 15; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
    |||||
Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 3
US-10-699-550-4
; Sequence 4, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 10724
; TYPE: DNA
; ORGANISM: Dengue virus type 2
US-10-699-550-4

Query Match          100.0%; Score 28; DB 18; Length 10724;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
    |||||
Db 136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 4
US-10-699-550-3
; Sequence 3, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 10735
; TYPE: DNA
; ORGANISM: Dengue virus type 1
US-10-699-550-3

Query Match          94.3%; Score 26.4; DB 18; Length 10735;
Best Local Similarity 96.4%; Pred. No. 0.083;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
    |||||
Db 134 AATATGCTGAAACGCGAGAGAAACCGCG 161

RESULT 5
US-09-840-707A-23
; Sequence 23, Application US/09840707A
; Patent No. US2002007276A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
; FILE REFERENCE: 24881-301C
; CURRENT APPLICATION NUMBER: US/09/840,707A
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: upper primer for Dengue virus type 2 detection

```

US-09-840-707A-23

Query Match 92.9%; Score 26; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCG 26
|||||
Db 1 AATATGCTGAAACGCGAGAGAAACCG 26

RESULT 6

US-10-038-557A-23
; Sequence 23, Application US/10038557A
; Publication No. US20030092684A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
; FILE REFERENCE: 24881-301D
; CURRENT APPLICATION NUMBER: US/10/038,557A
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 09/840,707
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: upper primer for Dengue virus type 2 detection
US-10-038-557A-23

Query Match 92.9%; Score 26; DB 14; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCG 26
|||||
Db 1 AATATGCTGAAACGCGAGAGAAACCG 26

RESULT 7

US-10-656-721-26
; Sequence 26, Application US/10656721
; Publication No. US20040265338A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Xiaowu
; APPLICANT: Dayton, Andrew I.
; APPLICANT: Zhang, Mingjie
; TITLE OF INVENTION: SUBGENOMIC REPLICONS OF THE FLAVIVIRUS
; TITLE OF INVENTION: DENGUE
; FILE REFERENCE: NIH202.001C1
; CURRENT APPLICATION NUMBER: US/10/656,721
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: PCT/US02/06962
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/274,684
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: 5' primer
US-10-656-721-26

Query Match 78.6%; Score 22; DB 18; Length 72;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAA 22
|||||
Db 28 AATATGCTGAAACGCGAGAGAA 49

RESULT 8

US-10-425-115-108018
; Sequence 108018, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 108018
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MMT4577_30008C.1
US-10-425-115-108018

Query Match 70.0%; Score 19.6; DB 18; Length 594;
Best Local Similarity 84.6%; Pred. No. 67;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGC 27
|||||
Db 552 ATATGCTGATTCCAGGAGAGAAACAGC 577

RESULT 9

US-10-363-345A-20593/c
; Sequence 20593, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 20593
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 20593
US-10-363-345A-20593

Query Match 67.9%; Score 19; DB 18; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGC 28
|||||

```
Db 325 ATACGCCGAACGCGAAGAAACGCG 299
RESULT 10
US-10-363-345A-20594
; Sequence 20594, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Pigenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363.345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 20594
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 20594
US-10-363-345A-20594
Query Match 67.9%; Score 19; DB 18; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAAACGCG 28
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 441 ATACGCCGAACGCGAAGAAACGCG 467

RESULT 11
US-10-369-493-32952/c
; Sequence 32952, Application US/10369493
; Publication No. US2003033675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 32952
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-369-493-32952
Query Match 67.1%; Score 18.8; DB 15; Length 1428;
Best Local Similarity 90.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CTGAACGCGAGAGAAACGCG 28
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1184 CGGAACGCGAGAGAAACGCG 1163

RESULT 12
US-10-156-761-2266
; Sequence 2266, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2266
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1602)
US-10-156-761-2266
Query Match 66.4%; Score 18.6; DB 15; Length 1602;
Best Local Similarity 84.0%; Pred. No. 2.1e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ATGCTGAACGCGAGAAACGCG 28
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 115 AGCTGCACCGCGAGAAACGCG 139

RESULT 13
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
Query Match 66.4%; Score 18.6; DB 15; Length 9025608;
Best Local Similarity 84.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ATGCTGAACGCGAGAAACGCG 28
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2778649 AGCTGCACCGCGAGAAACGCG 2778625
```

```
RESULT 14
US-10-042-991-11
; Sequence 11, Application US/10042991
; Publication No. US20020142407A1
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; FILE REFERENCE: 06027.0001U3
; CURRENT APPLICATION NUMBER: US/10/042,991
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-10-042-991-11
Query Match 65.7%; Score 18.4; DB 13; Length 1443;
Best Local Similarity 78.6%; Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 933 AATATGCTGAGATGCAAGAGAACTGAG 960

RESULT 15
US-10-422-323A-2/c
; Sequence 2, Application US/10422323A
; Publication No. US20040214178A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER, INC.
; TITLE OF INVENTION: REPORTER-SELECTABLE HEPATITIS C VIRUS REPLICON
; FILE REFERENCE: PC19102A (AG0190)
; CURRENT APPLICATION NUMBER: US/10/422,323A
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: 60/375,667
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/375,667
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 12305
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A cell line wherein the nucleic acid molecule is a self replicati
US-10-422-323A-2
Query Match 65.7%; Score 18.4; DB 18; Length 12305;
Best Local Similarity 78.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 9039 AATATGCTAAACGCGGCATACCCCGCG 9012

RESULT 16
US-10-422-323A-1/c
; Sequence 1, Application US/10422323A
; Publication No. US20040214178A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER, INC.
US-10-422-323A-1
; TITLE OF INVENTION: REPORTER-SELECTABLE HEPATITIS C VIRUS REPLICON
; FILE REFERENCE: PC19102A (AG0190)
; CURRENT APPLICATION NUMBER: US/10/422,323A
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: 60/375,667
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/375,667
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12315
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A cell line wherein the nucleic acid molecule is a self replicati
US-10-422-323A-1
Query Match 65.7%; Score 18.4; DB 18; Length 12315;
Best Local Similarity 78.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 9209 AATATGCTAAACGCGGCATACCCCGCG 9182

RESULT 17
US-09-238-076-5/c
; Sequence 5, Application US/09238076
; Patent No. US20020102540A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAPERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/238,076
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/034,756
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-238-076-5
```

```

Query Match      65.7%; Score 18.4; DB 9; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGGAGAGAAACCGCG 28
    ||||| ||||| ||||| ||||| |||||
Db 9714 AATATGCTAAACGCGGCATACCCCGCG 9687

RESULT 18
US-09-995-937-5/c
; Sequence 5, Application US/09995937
; Publication No. US20030028010A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
;
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/995,937
; FILING DATE: 28-May-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,756
; FILING DATE: 04-May-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-995-937-5

Query Match      65.7%; Score 18.4; DB 10; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGGAGAGAAACCGCG 28
    ||||| ||||| ||||| ||||| |||||
Db 9714 AATATGCTAAACGCGGCATACCCCGCG 9687

RESULT 19
US-09-917-563-5/c
; Sequence 5, Application US/09917563
; Publication No. US20030073080A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C

```

```

;
; VIRUS (HCV) AND USES THEREOF
;
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/917,563
; FILING DATE: 27-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/238,076
; FILING DATE: 26-JAN-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-917-563-5

Query Match      65.7%; Score 18.4; DB 10; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGGAGAGAAACCGCG 28
    ||||| ||||| ||||| ||||| |||||
Db 9714 AATATGCTAAACGCGGCATACCCCGCG 9687

RESULT 20
US-09-918-995-27460
; Sequence 27460, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27460
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(452)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27460

```

QY 1 AATATGCTGAAACGCGAGAGAAAC 24

Db 45 AATTGCGAAACTGGAGAGAAC 22

RESULT 25

US-10-198-846-3468/c

; Sequence 3468, Application US/10198846

; Publication No. US2003009974A1

; GENERAL INFORMATION:

; APPLICANT: Lillie, James

; APPLICANT: Xu, Yongyao

; APPLICANT: Wang, Youzhen

; APPLICANT: Steinmann, Kathleen

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

; TITLE OF INVENTION: THERAPY OF BREAST CANCER

; FILE REFERENCE: MRI-049

; CURRENT APPLICATION NUMBER: US/10/198,846

; CURRENT FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/306,220

; PRIOR FILING DATE: 2001-07-18

; NUMBER OF SEQ ID NOS: 14084

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3468

; LENGTH: 838

; TYPE: DNA

; ORGANISM: Homo sapiens

; NAME/KEY: misc feature

; LOCATION: 557, 616, 641, 691, 749, 765, 796, 815, 821

; OTHER INFORMATION: n = A,T,C or G

US-10-198-846-3468

Query Match 62.9%; Score 17.6; DB 14; Length 838;

Best Local Similarity 83.3%; Pred. No. 5.6e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAC 24

Db 108 AATTGCGAAACTGGAGAGAAC 85

RESULT 26

US-10-398-221-2508

; Sequence 2508, Application US/10398221

; Publication No. US20040018514A1

; GENERAL INFORMATION:

; APPLICANT: KUNST, Frederik

; APPLICANT: GLASER, Philippe

; TITLE OF INVENTION: Listeria innocua, genome and applications

; FILE REFERENCE: 344 702 - US

; CURRENT APPLICATION NUMBER: US/10/398,221

; CURRENT FILING DATE: 2003-03-27

; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061

; PRIOR FILING DATE: 2001-10-04

; PRIOR APPLICATION NUMBER: FR 00/12 697

; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 4025

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2508

; LENGTH: 945

; TYPE: DNA

; ORGANISM: Listeria innocua

US-10-398-221-2508

Query Match 62.9%; Score 17.6; DB 16; Length 945;

Best Local Similarity 83.3%; Pred. No. 5.7e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TATGCTGAAACGCGAGAGAACCG 26

Db 193 TATGCTGAAACACATGAGAAACAG 216

RESULT 27

US-10-398-221-2571

; Sequence 2571, Application US/10398221

; Publication No. US20040018514A1

; GENERAL INFORMATION:

; APPLICANT: KUNST, Frederik

; APPLICANT: GLASER, Philippe

; TITLE OF INVENTION: Listeria innocua, genome and applications

; FILE REFERENCE: 344 702 - US

; CURRENT APPLICATION NUMBER: US/10/398,221

; CURRENT FILING DATE: 2003-03-27

; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061

; PRIOR FILING DATE: 2001-10-04

; PRIOR APPLICATION NUMBER: FR 00/12 697

; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 4025

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2571

; LENGTH: 945

; TYPE: DNA

; ORGANISM: Listeria innocua

US-10-398-221-2571

Query Match 62.9%; Score 17.6; DB 16; Length 945;

Best Local Similarity 83.3%; Pred. No. 5.7e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TATGCTGAAACGCGAGAGAACCG 26

Db 193 TATGCTGAAACACATGAGAAACAG 216

RESULT 28

US-10-398-221-553

; Sequence 553, Application US/10398221

; Publication No. US20040018514A1

; GENERAL INFORMATION:

; APPLICANT: KUNST, Frederik

; APPLICANT: GLASER, Philippe

; TITLE OF INVENTION: Listeria innocua, genome and applications

; FILE REFERENCE: 344 702 - US

; CURRENT APPLICATION NUMBER: US/10/398,221

; CURRENT FILING DATE: 2003-03-27

; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061

; PRIOR FILING DATE: 2001-10-04

; PRIOR APPLICATION NUMBER: FR 00/12 697

; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 4025

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 553

; LENGTH: 966

; TYPE: DNA

; ORGANISM: Listeria innocua

US-10-398-221-553

Query Match 62.9%; Score 17.6; DB 16; Length 966;

Best Local Similarity 83.3%; Pred. No. 5.7e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TATGCTGAAACGCGAGAGAACCG 26

Db 214 TATGCTGAAACACATGAGAAACAG 237

RESULT 29

US-10-398-221-554

; Sequence 554, Application US/10398221

; Publication No. US20040018514A1

; GENERAL INFORMATION:

; APPLICANT: KUNST, Frederik

; APPLICANT: GLASER, Philippe

; TITLE OF INVENTION: Listeria innocua, genome and applications

; FILE REFERENCE: 344 702 - US

; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 554
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-554

Query Match 62.9%; Score 17.6; DB 16; Length 966;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TATGCTGAACGCGAGAGAAACCG 26
|||||
DB 214 TATGCTGAACACATGAGAAACG 237
|||||

RESULT 30
US-10-282-122A-29374/c
; Sequence 29374, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.03A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29374
; LENGTH: 1646
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-282-122A-29374

Query Match 62.9%; Score 17.6; DB 16; Length 1646;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TGCTGAACGCGAGAGAAACCGC 28
|||||
DB 210 TGAAGAAACGCGGGAACCGC 187
|||||

RESULT 31
US-08-319-974A-1/c
; Sequence 1, Application US/08319974A
; Publication No. US20030104576A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: Attenuated Viruses and Method of Making
; TITLE OF INVENTION: the Same
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Box 34009
; CITY: Charlotte
; STATE: No. US20030104576A1th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,974A
; FILING DATE: 07-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9718 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-319-974A-1

Query Match 62.9%; Score 17.6; DB 8; Length 9718;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATGCTGAACGCGAGAGAAACCGC 27
|||||
DB 4012 ATCTGCAACGCGAGATAATCGC 3989
|||||

RESULT 32
US-10-398-221-9
; Sequence 9, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04

```
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 684707
; TYPE: DNA
; ORGANISM: Listeria innocua
; NAME/KEY: misc feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
US-10-398-221-9

Query Match          62.9%; Score 17.6; DB 16; Length 684707;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TATGCTGAAACGCGAGAGAAACCG 26
Db 660685 TATGCTGAAACACATGAGAAACAG 660708

RESULT 33
US-10-398-221-9/c
; Sequence 9, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 684707
; TYPE: DNA
; ORGANISM: Listeria innocua
; NAME/KEY: misc feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
US-10-398-221-9

Query Match          62.9%; Score 17.6; DB 16; Length 684707;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TATGCTGAAACGCGAGAGAAACCG 26
Db 182545 TATGCTGAAACACATGAGAAACAG 182522

RESULT 34
US-10-398-221-2058/c
; Sequence 2058, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
US-10-398-221-9

Query Match          62.9%; Score 17.6; DB 16; Length 3011208;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TATGCTGAAACGCGAGAGAAACCG 26
Db 2434485 TATGCTGAAACACATGAGAAACAG 2434462

RESULT 35
US-10-767-701-19049/c
; Sequence 19049, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kowalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 19049
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3480-019-P1-K1-F12
US-10-767-701-19049

Query Match          62.1%; Score 17.4; DB 17; Length 341;
Best Local Similarity 77.8%; Pred. No. 6.2e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCG 27
Db 335 AAAAGGCTAAACACAGGAGAGAAACCG 309

RESULT 36
US-09-738-269-20/c
; Sequence 20, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: SYMES, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-09-738-269-20

Query Match          62.1%; Score 17.4; DB 10; Length 379;
```

Best Local Similarity 77.8%; Pred. No. 6.2e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAAACCGC 28
Db 59 ATATGCTGATAATAGAGAGAACCTGCG 33

RESULT 37
US-10-023-437-20/c
; Sequence 20, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEKKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID
; FILE REFERENCE: UTSID-736US
; CURRENT APPLICATION NUMBER: US/10/023,437
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-10-023-437-20

Query Match 62.1%; Score 17.4; DB 13; Length 379;
Best Local Similarity 77.8%; Pred. No. 6.2e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAAACCGC 28
Db 59 ATATGCTGATAATAGAGAGAACCTGCG 33

RESULT 38
US-10-437-963-17200
; Sequence 17200, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 17200
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(382)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22877C.1
US-10-437-963-17200

Query Match 62.1%; Score 17.4; DB 17; Length 382;

Best Local Similarity 77.8%; Pred. No. 6.2e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGC 27
Db 79 AATTGTCTGGAAGCGGACAAAACCCAC 105

RESULT 39
US-10-424-599-53946/c
; Sequence 53946, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 53946
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_19726C.1
US-10-424-599-53946

Query Match 62.1%; Score 17.4; DB 16; Length 528;
Best Local Similarity 77.8%; Pred. No. 6.5e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAAACCGC 28
Db 294 ATATCCAAAACGCGAGAGAGACGCG 268

RESULT 40
US-10-027-632-237136/c
; Sequence 237136, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237136
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature

```
; LOCATION: (1)...(558)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-237136

Query Match      62.1%; Score 17.4; DB 13; Length 558;
Best Local Similarity 77.8%; Pred. No. 6.5e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAACCGC 27
    ||||| ||||| ||||| ||||| |||||
Db 263 AATATGCTGAAGAGGGATATAAACCGC 237

RESULT 41
US-10-027-632-237136/c
; Sequence 237136, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/145,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237136
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(558)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-237136

Query Match      62.1%; Score 17.4; DB 15; Length 558;
Best Local Similarity 77.8%; Pred. No. 6.5e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAACCGC 27
    ||||| ||||| ||||| ||||| |||||
Db 263 AATATGCTGAAGAGGGATATAAACCGC 237

RESULT 42
US-10-363-345A-34197/c
; Sequence 34197, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712

Query Match      62.1%; Score 17.4; DB 18; Length 589;
Best Local Similarity 77.8%; Pred. No. 6.6e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATATGCTGAACCGGAGAGAAACCGCG 28
    ||| ||||| ||||| ||||| |||||
Db 166 ATACCGGAAACGCGAAAAAAACCGCG 140

RESULT 43
US-10-363-345A-34198
; Sequence 34198, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 34198
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-34198

Query Match      62.1%; Score 17.4; DB 18; Length 589;
Best Local Similarity 77.8%; Pred. No. 6.6e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATATGCTGAACCGGAGAGAAACCGCG 28
    ||| ||||| ||||| ||||| |||||
Db 424 ATACCGGAAACGCGAAAAAAACCGCG 450

RESULT 44
US-10-363-345A-38631/c
; Sequence 38631, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 38631
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-38631
```


; TYPE: DNA
; ORGANISM: Salmonella paratyphi A
US-10-282-122A-36749

Query Match 62.1%; Score 17.4; DB 16; Length 778;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGC 27
||||| ||||| ||||| ||||| |||||
Db 525 AATACGCTGAACGCGAGAGATTAATCGC 499

RESULT 48
US-10-011-033-11
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; McMaster, J. Russell
; Tricoli, David M
; Reynolds, John F
; Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; Cucurbit Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Ver. 1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011.033
; FILING DATE: 13-No. US20020124286A1-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/875.233
; FILING DATE: 26-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; JOURNAL: J. Gen. Virol.
; VOLUME: 70
; PAGES: 1065-1073
; DATE: 1989

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-011-033-11

Query Match 62.1%; Score 17.4; DB 13; Length 983;
Best Local Similarity 77.8%; Pred. No. 7e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGC 28
| ||||| ||||| ||||| ||||| |||||
Db 113 AGATGCTGAAACTCAATAGAACCTCG 139

RESULT 49
US-09-738-269-22/c
; Sequence 22, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-09-738-269-22

Query Match 62.1%; Score 17.4; DB 10; Length 2520;
Best Local Similarity 77.8%; Pred. No. 7.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGC 28
||||| ||||| ||||| ||||| |||||
Db 1856 ATATGCTGATAATAGAGAACCTGCG 1830

RESULT 50
US-10-023-437-22/c
; Sequence 22, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID
; AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
; FILE REFERENCE: UTSD:736US
; CURRENT APPLICATION NUMBER: US/10/023,437
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-10-023-437-22

Query Match 62.1%; Score 17.4; DB 13; Length 2520;
Best Local Similarity 77.8%; Pred. No. 7.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGC 28
||||| ||||| ||||| ||||| |||||
Db 1856 ATATGCTGATAATAGAGAACCTGCG 1830

Search completed: January 19, 2005, 13:58:54
Job time : 223 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 12:51:42 ; Search time 1550 Seconds
(without alignments)
658.266 Million cell updates/sec

Title: US-10-085-944-2
Perfect score: 28
Sequence: 1 aatatgtgaacgagagaaaccgag 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20.6	73.6	776	7	CF996467
C 2	19.8	70.7	720	7	CF455745
C 3	19.6	70.0	301	6	CB078143
C 4	19.6	70.0	712	7	CF372439
C 5	19.6	70.0	722	7	CF512147
C 6	19.6	70.0	734	7	CF512236
C 7	19.4	69.3	464	2	BE841207
C 8	19	67.9	520	9	CR305770
C 9	19	67.9	559	9	TA262H01Q
C 10	19	67.9	568	8	AQ945692
C 11	19	67.9	576	9	TA140D12P
C 12	19	67.9	580	2	BE776235
C 13	19	67.9	602	1	AL673619
C 14	19	67.9	629	1	AL647632
C 15	19	67.9	633	6	CA349616
C 16	19	67.9	649	6	CA356841
C 17	19	67.9	738	9	AG363192
C 18	19	67.9	768	9	CC504335
C 19	19	67.9	870	9	AG186531
C 20	19	67.9	988	7	CF995511
C 21	18.8	67.1	1687	2	BF128456
C 22	18.6	66.4	407	6	CF198531
C 23	18.6	66.4	456	4	BG659286
C 24	18.6	66.4	563	7	CF939381

25	18.6	66.4	584	8	AQ657703
26	18.6	66.4	593	9	FR0021761
C 27	18.6	66.4	636	7	CO300868
28	18.6	66.4	640	7	CN876173
29	18.6	66.4	642	1	AI135620
30	18.6	66.4	671	7	CN882707
31	18.6	66.4	675	7	CN879811
32	18.6	66.4	683	7	CN918097
C 33	18.6	66.4	684	8	AQ657387
34	18.6	66.4	799	9	CL527496
35	18.4	65.7	427	9	CG016439
C 36	18.4	65.7	456	8	AQ724090
37	18.4	65.7	496	2	AW599272
C 38	18.4	65.7	582	8	BZ130571
39	18.4	65.7	655	6	CB020289
C 40	18.4	65.7	672	8	BH100535
41	18.4	65.7	675	6	CA112278
C 42	18.4	65.7	695	8	BH929269
C 43	18.4	65.7	697	8	BH549312
44	18.4	65.7	743	7	CK326303
45	18.4	65.7	750	2	BB615972
C 46	18.4	65.7	774	8	BZ154086
C 47	18.4	65.7	788	8	BZ132164
48	18.4	65.7	790	2	BF678988
49	18.4	65.7	792	4	B1753870
C 50	18.4	65.7	824	2	BF620613

ALIGNMENTS

RESULT 1
CF996467/c

LOCUS

DEFINITION AGENCOURT 16394292 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7037741
5', mRNA sequence.

ACCESSION CF996467

VERSION CF996467.1

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 776)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@remail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: L1AM14788 row: e column: 03
High quality sequence stop: 734.

FEATURES

source

Location/Qualifiers
1..776
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7037741"
/tissue_type="whole body"
/lab_host="DH10B"
/clone_lib="NIH_ZGC_7"
/note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
Bulk tissue was collected from a whole adult individual"

from the Tuebingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1. Library was size-selected for >1 kb fragments and normalized. A non-normalized version of this library is also available (NIH_ZGC_10). Library was constructed by Open Biosystems (Huntsville, AL)"

ORIGIN

Query Match 73.6%; Score 20.6; DB 7; Length 776;
Best Local Similarity 85.2%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAACCGCG 28
|||
Db 549 ATGTGCTGACACGCGAGAGACCGG 523
|||

RESULT 2

CF455745

LOCUS

DEFINITION AGENCOURT 15376947 Lupski anterior_horn Homo sapiens cDNA clone IMAGE:30515857 5', mRNA sequence. EST 04-SEP-2003

ACCESSION

CF455745

VERSION

CF455745.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 720)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Invitrogen Corp
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: NDAM581 row: k column: 02
High quality sequence start: 194
High quality sequence stop: 544.

FEATURES

source

1..720
/location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30515857"
/tissue_type="Peripheral Nervous system"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="Lupski anterior horn"
/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb. Library was constructed by Invitrogen and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine)."

ORIGIN

Query Match 70.7%; Score 19.8; DB 7; Length 720;
Best Local Similarity 91.3%; Pred. No. 3.1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAA 23
|||
Db 189 AAGATGCTGAACACGAGAGAAA 211
|||

RESULT 3

CB078143

LOCUS

DEFINITION

CB078143

ACCESSION

CB078143

VERSION

CB078143.1

KEYWORDS

EST.

SOURCE

Hedvotis terminalis

ORGANISM

Hedvotis terminalis

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2003)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Plate: hj63 row: h column: 04

Seq primer: -21M13Univrev

High quality sequence stop: 301.

Location/Qualifiers

1..301

/organism="Hedvotis terminalis"

/mol_type="mRNA"

/db_xref="taxon:219667"

/clone="hj63h04"

/dev_stage="pre-anthesis; Stage 2"

/clone_lib="Hedvotis terminalis flower - Stage 2 (NYBG)"

/note="Organ: flower; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date: Completed 12/18/01. Submitted to CSHL 12/21/01 Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: collected on the island of Hawaii, Hawaii; NYBG herbarium voucher TM2562"

ORIGIN

Query Match 70.0%; Score 19.6; DB 6; Length 301;
Best Local Similarity 84.6%; Pred. No. 3.7e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy

3

TATGCTGAAACGCGAGAGAACCGCG 28

|||

Db

212

TATGCTGAAACGCGAGAGAACCGCG 237

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|||

|||

|||

TITLE Expressed sequence tags from the grapevine cultivar Cabernet Sauvignon

JOURNAL Unpublished (2003)

COMMENT Contact: Mark R. Thomas
CSIRO Plant Industry
CSIRO
PO Box 350, Glen Osmond, SA, 5064, Australia
Tel: 61 8 83038600
Fax: 61 8 83038601
Email: Mark.R.Thomas@csiro.au
Seq primer: CCCAGTCACGACGGTGTAAAAACG (M13 Forward)
POLYA=Yes.

FEATURES

source	Location/Qualifiers
	1..712
	/organism="Vitis vinifera"
	/mol_type="mRNA"
	/cultivar="Cabernet Sauvignon"
	/db_xref="taxon:29760"
	/clone="CSEC5052D08"
	/sex="Hermaphrodite"
	/dev_stage="12 - modified E-L system"
	/clone_lib="CabSau Normalised Flower stage 12 (FLN001012)"
	/notes="Organ: Inflorescence including flowers; Vector: pZL; Normalised cDNA library from immature inflorescences at stage 12 of the modified E-L system. Tissue collected from field grown plants. A description of the modified E-L system can be found in the paper by B. G. Coombe 'Adoption of a system for identifying grapevine growth stages' (1995) Aust. J. Grape and Wine Res. 1: 104-110."

ORIGIN

Query Match	70.0%;	Score 19.6;	DB 7;	Length 712;
Best Local Similarity	84.6%;	Pred. No. 3.9e+02;		
Matches	22;	Conservative 0;	Mismatches 4;	Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGCAGAGAACC 26
| | | | | | | | | | | | | | | |
Dd 374 ATTATGCTGAAGACTCGAAGAACTG 399

RESULT 5

CF512147/c

LOCUS CF512147.1 GI:34543915

DEFINITION 722 bp mRNA linear EST 09-SEP-2003

Cabud0003 IF A10 Vitis vinifera cv. cabernet sauvignon (Clone 8)

Bud - CABUD Vitis vinifera cDNA clone Cabud0003_IF_A10_5', mrna sequence.

ACCESSION CF512147

VERSION CF512147.1

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.

1 (bases 1 to 722)

Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J., Jones,K. and Cook,D.

REFERENCE Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'

AUTHORS berries at various developmental stages

TITLE Unpublished (2003)

JOURNAL Contact: Douglas Cook, PhD

COMMENT CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.

FEATURES

source	Location/Qualifiers
	1..722
	/organism="Vitis vinifera"
	/mol_type="mRNA"
	/cultivar="Cabernet Sauvignon (Clone 8)"

'Cabernet Sauvignon' Clone 8 dissected buds. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-veraison. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
 5'-AAGCAGTGGTATCAACGCGAGAGTGGCCATTTACGCCGGG-3' and
 5'-ATTATAGAGCGGAGCGGCGGCATG-DT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 70.0%; Score 19.6; DB 7; Length 734;
 Best Local Similarity 84.6%; Pred. No. 3.9e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAACCG 26
 Db 373 ACTATGCTGAAACTCGAAGAACTG 398

RESULT 7

BE841207/c
 LOCUS BE841207 464 bp mRNA linear EST 22-SEP-2000
 DEFINITION QV4-SN0024-200700-304-a07 SN0024 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BE841207
 VERSION BE841207.1 GI:10273585
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

PUBMED 20202663

10737800

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV4-SN0024-200700-304-a07&t3=2000-07-20&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 10

High quality sequence stop: 248.

FEATURES

source

1. .464
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="SN0024"
 /note="Organ: stomach_normal; Vector: puc18; Site:1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under

ORIGIN

low stringency conditions."
 Query Match 69.3%; Score 19.4; DB 2; Length 464;
 Best Local Similarity 95.2%; Pred. No. 4.6e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TGCTGAAACGCGAGAGAACCG 25
 Db 329 TGCTGAAAGCGAGAGAACCG 309

RESULT 8

CR305770
 LOCUS CR305770 520 bp DNA linear GSS 01-MAR-2004
 DEFINITION Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago truncatula, genomic survey sequence.

ACCESSION CR305770

VERSION CR305770.1 GI:44851914

KEYWORDS GSS.

SOURCE Medicago truncatula (barrel medic)

ORGANISM

Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE 1 (bases 1 to 520)

Genoscope.

Direct Submission

TITLE Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :

JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

FEATURES

source

1. .520
 /location/Qualifiers
 /organism="Medicago truncatula"
 /mol_type="genomic DNA"
 /cultivar="Jemalong A17"
 /db_xref="taxon:3880"
 /clone_lib="MTE1"
 /note="Vector: pindigobac ; Site 1: EcoRI ; Site 2: EcoRI ; Debelle F. and Chalhou B.-Genoscope sequence ID : mtel-25N13RM1"

ORIGIN

Query Match 67.9%; Score 19; DB 9; Length 520;
 Best Local Similarity 81.5%; Pred. No. 7.1e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAACCGC 27
 Db 241 AACAGGCTGCAACGCGAAGAACCGC 267

RESULT 9

TA262H01Q
 LOCUS TA262H01Q 559 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 262h01, reverse sequence, genomic survey sequence.

ACCESSION AL487728

VERSION AL487728.1 GI:11850764

KEYWORDS GSS.

SOURCE Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 559)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajadream, M.A. and Barrell, B.G.

TITLE

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and


```

BE776235
LOCUS       BE776235          580 bp      mRNA          linear      EST 20-SEP-2000
DEFINITION  MY-12-F-04 PinfestansMY Phytophthora infestans cDNA, mRNA sequence.
ACCESSION   BE776235
VERSION     BE776235.1      GI:10229890
KEYWORDS    EST.
SOURCE      Phytophthora infestans (potato late blight agent)
            Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1 (bases 1 to 580)
AUTHORS    Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.
TITLE       Initial assessment of gene diversity for the oomycete pathogen
            Phytophthora infestans based on expressed sequences
JOURNAL     Fungal Genet. Biol. 28 (2), 94-106 (1999)
MEDLINE     20056376
PUBMED      10587472
COMMENT     Contact: Govers F
            Laboratory of Phytopathology
            Wageningen University
            Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
            Tel: 31 317 483 138
            Fax: 31 317 483 412
            Email: Francine.Govers@medew.fyto.wau.nl.
FEATURES             Location/Qualifiers
     source          1..580
                     /organism="Phytophthora infestans"
                     /mol_type="mRNA"
                     /strain="DDR7602, A1 mating type"
                     /db_xref="taxon:4787"
                     /dev_stage="4-week old vegetative, non-sporulating
                     mycelium in synthetic medium"
                     /lab_host="E. coli, strain DHS-alpha"
                     /clone_lib="PinfestansMY"
                     /notes="vector: pSPORT1; Site 1: SalI; Site 2: NotI; Total
                     RNA was isolated from mycelium of P. infestans DDR7602
                     cultured for 4 weeks in synthetic medium. EST clones were
                     named by their position in the microtiter plate, preceded
                     by the prefix MY (for mycelial) and the successive number
                     of the microtiter plate (e.g. MY-06-A-04)."
```

```

ORIGIN
Query Match       67.9%; Score 19; DB 1; Length 602;
Best Local Similarity 81.5%; Pred. No. 7.1e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2  ATATGCTGAAACGCGAGAAACCGCG 28
      ||| ||||| ||||| ||||| |||||
Db   202 ATAAAGCTGAAAGCGGAGAGAAACGCG 228

RESULT 14
AL647632
LOCUS       AL647632          629 bp      mRNA          linear      EST 20-NOV-2003
DEFINITION  AL647632 XGC-gastrula Xenopus tropicalis cDNA clone TGas037f09 5',
            mRNA sequence.
ACCESSION   AL647632
VERSION     AL647632.2      GI:38458607
KEYWORDS    EST.
ORGANISM    Xenopus tropicalis (western clawed frog)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1 (bases 1 to 629)
AUTHORS    Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE       Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL     Unpublished (2003)
COMMENT     On Dec 13, 2001 this sequence version replaced gi:17655942.
            Contact: Huckle E
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dt primed from Sug of poly A+ RNA from stages 10-13
            gastrulae. EcorI-NotI cut cDNA was then ligated into pCS107 with
            EcorI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site 1: EcorI; Site 2: NotI
            Host: Escherichia coli XL1-blue
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TGas037f09.plkSP6
            Sequencing primer: SP6.
FEATURES             Location/Qualifiers
     source          1..629
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TGas037f09"
                     /dev_stage="gastrula (stages 10.5-12 mixed)"
```

/lab host="Escherichia coli XL1-blue"
/clone lib="XGC-gastrula"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dr primed from Sug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

ORIGIN

Query Match 67.9%; Score 19; DB 1; Length 629;
Best Local Similarity 81.5%; Pred. No. 7.2e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2 AATATGCTGAACCGGAGAGAAACCGC 28

Db 234 AATAGCTGAACCGGAGAGAAACGTG 260

RESULT 15

CA349616 633 bp mRNA linear EST 05-NOV-2002

LOCUS 620082 NCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT142M04_C G02

DEFINITION 5', mRNA sequence.

ACCESSION CA349616

VERSION CA349616.1 GI:24594787

KEYWORDS EST.

SOURCE Oncorhynchus mykiss (rainbow trout)

ORGANISM

Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE

AUTHORS 1 (bases 1 to 633)
Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,
Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.

TITLE Sequence analysis of a rainbow trout cDNA library and creation of a

JOURNAL

COMMENT CytoGenet. Genome Res. 102 (1-4), 347-354 (2003)

Contact: Rexroad CE

USDA, ARS, National Center for Cool and Cold Water Aquaculture

11876 Leetown Road, Kearneysville, WV 25430, USA

Tel: 304 724 8340 x2129

Fax: 304 725 0351

Email: crexroadnccwa.ars.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_alt option. Vector identified by

cross_match v0.990329.

Seq primer: AGCGATAACAATTTCACACAGGA.

FEATURES

source

1..633

/organism="Oncorhynchus mykiss"

/mol_type="mRNA"

/db_xref="taxon:8022"

/clone="1RT142M04_C G02"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="NCCWA 1RT"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;

Library made from pooled tissue from brain, gill, liver,

spleen, muscle, and kidney."

ORIGIN

Query Match 67.9%; Score 19; DB 6; Length 633;
Best Local Similarity 81.5%; Pred. No. 7.2e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 AATATGCTGAACCGGAGAGAAACCGC 27

Db 579 AATATGCAAGAACTCGAGAGAAGCTGC 605

RESULT 16

CA356841 649 bp mRNA linear EST 05-NOV-2002

LOCUS

DEFINITION

629106 NCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT100M13_A_G07
5', mRNA sequence.

ACCESSION CA356841

VERSION CA356841.1 GI:24602028

KEYWORDS EST.

SOURCE Oncorhynchus mykiss (rainbow trout)

ORGANISM

Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE

AUTHORS

1 (bases 1 to 649)
Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,
Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.

TITLE Sequence analysis of a rainbow trout cDNA library and creation of a

JOURNAL

COMMENT CytoGenet. Genome Res. 102 (1-4), 347-354 (2003)

Contact: Rexroad CE

USDA, ARS, National Center for Cool and Cold Water Aquaculture

11876 Leetown Road, Kearneysville, WV 25430, USA

Tel: 304 724 8340 x2129

Fax: 304 725 0351

Email: crexroadnccwa.ars.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_alt option. Vector identified by

cross_match v0.990329.

Seq primer: AGCGATAACAATTTCACACAGGA.

FEATURES

source

1..649

/organism="Oncorhynchus mykiss"

/mol_type="mRNA"

/db_xref="taxon:8022"

/clone="1RT100M13_A_G07"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="NCCWA 1RT"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;

Library made from pooled tissue from brain, gill, liver,

spleen, muscle, and kidney."

ORIGIN

Query Match 67.9%; Score 19; DB 6; Length 649;
Best Local Similarity 81.5%; Pred. No. 7.2e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 AATATGCTGAACCGGAGAGAAACCGC 27

Db 469 AATATGCAGAACTCGAGAGAAGCTGC 495

RESULT 17

AG363192/c

LOCUS

DEFINITION AG363192 738 bp DNA linear GSS 03-JUN-2004

Mus musculus molossinus DNA, clone:MSMg01-164N14.TJ, genomic survey

sequence.

ACCESSION AG363192

VERSION AG363192.1 GI:47974397

KEYWORDS GSS.

SOURCE Mus musculus molossinus

ORGANISM

Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

1 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

BAC end Sequences of Library MSMg01

Unpublished

2 (bases 1 to 738)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail: hattori@gscc.riken.jp, URL: http://hgp.gscc.riken.go.jp/,

Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT Clones are derived from the mouse BAC library MSNg01. For BAC library availability, please contact Kuniya Abe (abe@c.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@c.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
FEATURES Location/Qualifiers
source
1. 738
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clones="MSNg01-164N14.TJ"
/sex="male"
/tissue types="mixture of kidney and spleen"
/clone_lib="MSNg01 Mouse Male BAC Library"
ORIGIN
Query Match 67.9%; Score 19; DB 9; Length 738;
Best Local Similarity 81.5%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 AATATGCTGAACCGAGAGAAACCGC 27
||||| ||||| ||||| ||||| |||||
Db 690 AATATACCGAAACCGAGGGAACCGC 664
RESULT 18
CC504335
LOCUS CH240_344G2.T7 CHORI-240 Bos taurus genomic clone CH240_344G2,
DEFINITION genomic survey sequence.
VERSION CC504335.1 GI:31822628
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 768)
AUTHORS Holt,R., Stott,J., Yang,G., Barber,S., Smalrus,D., Prabhu,A.-L.,
Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Narra,M., de Jong,P., McWilliam,S., Barris,W.,
Dairymple,B.P. and Tellam,R.
TITLE Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
JOURNAL Unpublished (2003)
COMMENT Other GSSs: CH240_344G2.TARBAC13P2
Contact: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bccsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orderinginformation.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Science Centre, Canada.
Plate: 344 row: G column: 2

Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. 768
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_344G2"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site.1: MboI; Site.2: MboI;
Hereford bull LI Domino 99375; CHORI-240 Bovine BAC
Library (Male) produced by Pieter de Jong"
ORIGIN
Query Match 67.9%; Score 19; DB 9; Length 768;
Best Local Similarity 81.5%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 ATATGCTGAACCGAGAGAAACCGC 28
||||| ||||| ||||| ||||| |||||
Db 86 ATGTACAGAAACGTGAGAAACACG 112
RESULT 19
AG186531/c
LOCUS Pan troglodytes DNA, clone: RP43-060P05.TJ, genomic survey
DEFINITION sequence.
ACCESSION AG186531
VERSION AG186531.1 GI:16716211
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
Unpublished
2 (bases 1 to 870)
TITLE Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
JOURNAL Direct Submission
COMMENT Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
FEATURES Location/Qualifiers
source
1. 870
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-060P05.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
ORIGIN
Query Match 67.9%; Score 19; DB 9; Length 870;

```

Best Local Similarity 81.5%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAACCGGAGAGAAACCGC 28
||||| ||||| ||||| ||||| |||||
Db 690 ATATCGGAATCGGAGAGCAACGCG 664

RESULT 20
CF995511/c
LOCUS CF995511 988 bp mRNA linear EST 25-NOV-2003
DEFINITION AGNCOURT 16028690 NIH MGC 217 Homo sapiens CDNA clone
IMAGE:30524078 5', mRNA sequence.
ACCESSION CF995511
VERSION CF995511.1 GI:38512120
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 988)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM603 row: a column: 15
High quality sequence stop: 407.
Location/Qualifiers
1..988
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30524078"
/tissue_type="Pooled Chondrosarcoma Tumor cells"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 217"
/note="Vector: pYX-Asc; Site 1: EcoRI; Site 2: NotI;
Library is oligo-dT primed and directionally cloned.
Denatured RNA was size fractionated on a 1% agarose gel.
First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. Average insert size
0.5-1kb. Adaptors 5' (AATTCGGCAGG)3' and 5'd
(CCTGTCGGC)3'. 3' Linker sequence - CGCGCGCTGAGAGCC T18.
Sequencing primers 3'end: T3 promoter primer 5'd
(ATTACCCCTCACTAAGGGA)3', 5' End: T7 promoter primer 5'd
(TAATACACCTCACTATAGG)3'. Average insert size 0.5-1kb.
Library was constructed in the laboratory of M. Bento
Soares. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 67.9%; Score 19; DB 7; Length 988;
Best Local Similarity 81.5%; Pred. No. 7.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAACCGC 27
||||| ||||| ||||| ||||| |||||
Db 727 ATTATGCGGAACGAGAGATTACCGC 701

Best Local Similarity 81.5%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAACCGGAGAGAAACCGC 28
||||| ||||| ||||| ||||| |||||
Db 690 ATATCGGAATCGGAGAGCAACGCG 664

RESULT 21
BF128456
LOCUS BF128456 1687 bp mRNA linear EST 24-OCT-2000
DEFINITION 601810142R1 NIH_MGC_46 Homo sapiens CDNA clone IMAGE:4053059 3',
mRNA sequence.
ACCESSION BF128456
VERSION BF128456.1 GI:10967496
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1687)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM891 row: c column: 12
High quality sequence start: 26
High quality sequence stop: 165.
Location/Qualifiers
1..1687
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4053059"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 67.1%; Score 18.8; DB 2; Length 1687;
Best Local Similarity 90.9%; Pred. No. 9.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTGAACCGGAGAGAAACCGC 28
||||| ||||| ||||| ||||| |||||
Db 694 CAGACACCGGAGAGAAACCGC 715

RESULT 22
CF198531/c
LOCUS CF198531 407 bp mRNA linear EST 01-AUG-2003
DEFINITION EST0126 Tamarix androssowii leaf Tamarix androssowii CDNA, mRNA
sequence.
ACCESSION CF198531
VERSION CF198531.1 GI:33392904
KEYWORDS EST.
SOURCE Tamarix androssowii
ORGANISM Tamarix androssowii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Tamaricaceae; Tamarix.
REFERENCE 1 (bases 1 to 407)
AUTHORS Wang, Y., Yang, C., Jiang, J., Liu, G., Wu, J. and Liu, Z.
TITLE EST acquired from cDNA library of Tamarix androssowii treated with

```


NaHCO₃
 Unpublished (2003)
 Contact: Yucheng Wang
 Forestry Source and Environment College
 Northeast Forestry University
 Hexing 26, Harbin, Heilongjiang, 150040, P.R. China
 Tel: 086-451-2190607
 Email: WANGYUCHENG1029@YAHOO.COM.CN.

FEATURES
 source
 1. .407
 /organism="Tamarix androssowii"
 /mol_type="mRNA"
 /db_xref="taxon:189785"
 /tissue_type="leaf"
 /clone_lib="Tamarix androssowii leaf"

ORIGIN
 Query Match 66.4%; Score 18.6; DB 6; Length 407;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAC 25
 ||||| ||||| ||||| ||||| |||||
 Db 328 AATATGCTTGAAGGAGAGAGAAC 304
 ||||| ||||| ||||| ||||| |||||

RESULT 23
 BG659286/c
 LOCUS
 DEFINITION TgESTya21d01.y1 TgVEG118 Tachyzoite cDNA Library Toxoplasma gondii
 cDNA clone TgESTya21d01.y1 5' similar to TR:081505 O81505 F9D12.1
 PROTEIN. i, mRNA sequence.

ACCESSION BG659286
 VERSION BG659286.1 GI:13801535
 KEYWORDS EST.
 SOURCE Toxoplasma gondii
 ORGANISM Toxoplasma gondii
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Sarcocystidae; Toxoplasma.
 1 (bases 1 to 456)
 Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioke, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
 Toxoplasma EST Project
 Unpublished (2001)
 Contact: Clifton, S.
 Toxoplasma EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: toxo@watson.wustl.edu
 Contact David Sibley (toxoeest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.
 Seq primer: -40RP from Gibco
 High quality sequence stop: 408.

FEATURES
 source
 1. .456
 /organism="Toxoplasma gondii"
 /mol_type="mRNA"
 /strain="VEG"
 /db_xref="taxon:5811"
 /clone="TgESTya21d01.y1"
 /dev_stage="Tachyzoite"
 /lab_host="DH10B"
 /clone_lib="TgVEG118 Tachyzoite cDNA Library"
 /note="Vector: pBluescript SK; Site 1: EcoRI; Site 2: xhoI; This library was constructed by Kelian Tang, Robert Cole, and L. David Sibley at Washington University. cDNAs were synthesized from poly(A)+ RNA by oligo(dT) priming, size-selected and directionally cloned into the Uni-ZAP XR

lambda vector (Stratagene). The primary library was mass excised as phagemids and rescued in SOLR cells. The plasmid library was recovered from the SOLR cells and transformed in mass into DH10B (GeneHog, Research Genetics, Inc.) for sequencing. WARNING: This library may contain a small percentage contaminants from human fibroblast cells."

ORIGIN
 Query Match 66.4%; Score 18.6; DB 4; Length 456;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAACCG 26
 ||||| ||||| ||||| ||||| |||||
 Db 435 ATATCTGAAATGCGAGATACAG 411
 ||||| ||||| ||||| ||||| |||||

RESULT 24
 CF939381/c
 LOCUS
 DEFINITION NCESTgab57g05.y1 Nc-1 Tachyzoite cDNA Library 2 Neospora caninum
 cDNA 5' similar to SW:YC27_HUMAN Q9Y316 HYPOTHETICAL PROTEIN
 CGI-27, mRNA sequence.

ACCESSION CF939381
 VERSION CF939381.1 GI:38438622
 KEYWORDS EST.
 SOURCE Neospora caninum
 ORGANISM Neospora caninum
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Sarcocystidae; Neospora.
 1 (bases 1 to 563)
 Cole, R., Fogarty, S., Tang, K., Howe, D.K., Sibley, L.D., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wyllie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Ronko, I., Tsagareishvili, R., Fedele, M., Belaygorod, L., Franklin, C., Teagareishvili, R., Maguire, L., Wadkins, J., Richey, J., Waterston, R. and Wilson, R.
 USDA-WashU Neospora EST Project
 Unpublished (2000)
 Contact: Sandy Clifton, Ph.D. - Neospora
 USDA-WashU Neospora EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Contact David Sibley (toxoeest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.
 Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1. .563
 /organism="Neospora caninum"
 /mol_type="mRNA"
 /db_xref="taxon:29176"
 /dev_stage="Tachyzoite"
 /lab_host="GC10 Competent Cells(PGC)"
 /clone_lib="Nc-1 Tachyzoite cDNA Library 2"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: xhoI; The cDNA library was constructed by Kelian Tang, and Robert Cole at Washington University. cDNA was synthesized from poly mRNA using an oligo-dT primer containing a xhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA, and products were size-selected on sephacryl S500. The cDNA were directionally cloned into the EcoRI/xhoI prepared pBluescript II SK+ vector, and electroporated into GC10 Competent Cells(PGC). The library may contain a small percentage of host or bacterial contaminants."

FEATURES
 source
 1. .563
 /organism="Neospora caninum"
 /mol_type="mRNA"
 /db_xref="taxon:29176"
 /dev_stage="Tachyzoite"
 /lab_host="GC10 Competent Cells(PGC)"
 /clone_lib="Nc-1 Tachyzoite cDNA Library 2"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: xhoI; The cDNA library was constructed by Kelian Tang, and Robert Cole at Washington University. cDNA was synthesized from poly mRNA using an oligo-dT primer containing a xhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA, and products were size-selected on sephacryl S500. The cDNA were directionally cloned into the EcoRI/xhoI prepared pBluescript II SK+ vector, and electroporated into GC10 Competent Cells(PGC). The library may contain a small percentage of host or bacterial contaminants."

ORIGIN
 Query Match 66.4%; Score 18.6; DB 7; Length 563;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATGCTGAACGCGAGAGAACCGG 28
 Db 332 ATGCTGAACGAGAGAGAACCGG 308

RESULT 25
 A0657703
 LOCUS

DEFINITION
 Sheared DNA-21N17.TR Sheared DNA Trypanosoma brucei genomic clone

ACCESSION
 A0657703

VERSION
 A0657703.1 GI:5165471

KEYWORDS
 GSS.

SOURCE
 Trypanosoma brucei

ORGANISM
 Trypanosoma brucei

REFERENCE
 1 (bases 1 to 584)

AUTHORS
 El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
 Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S.,
 Donelson,J., Fraser,C. and Adams,M.

TITLE
 Determination of clone end sequences from Trypanosoma brucei GUTat

JOURNAL
 10.1 sheared DNA library

COMMENT
 Unpublished (1999)

Other_GSSs: Sheared DNA-21N17.TF

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: nelsayed@tigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared

DNA library constructed at TIGR. Clones will be available for

distribution through ATCC. Sheared DNA end sequences search page:

http://www.tigr.org/cdb/mb/tbdb/.

Seq primer: M13-Reverse

Class: shotgun.

Location/Qualifiers

1..584

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927/4 GUTat 10.1"

/db_xref="taxon:5691"

/clone="Sheared DNA-21N17"

/clone_lib="Sheared DNA"

/note="Vector: pUC18; Site_1: SmaI; Constructed at The

Institute for Genomic Research (TIGR), Rockville, MD.

Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically

sheared to give a tight size distribution (approx 2 kb).

The v + i method used for the library construction is

described in detail in Smith, H.O. and Venter, J.C.

(Making small insert libraries for whole genome shotgun

sequencing projects. In Genome Sequencing: A Practical

Approach, eds. M. Vaudin and B. Barell, Oxford University

Press, 1999)."

Query Match 66.4%; Score 18.6; DB 8; Length 584;

Best Local Similarity 84.0%; Pred. No. 1.1e+03;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAACCC 25

Db 12 AATATCTCTGAACGCGAGAGAACCC 36

RESULT 26

FR0021761

LOCUS

FR0021761

593 bp DNA linear GSS 25-FEB-2004

DEFINITION
 F.rubripes GSS sequence, clone 067111bD11, genomic survey sequence.

ACCESSION
 AL014632

VERSION
 AL014632.1 GI:2681000

KEYWORDS
 GSS; genome survey sequence.

SOURCE
 Takifugu rubripes (Fugu rubripes)

ORGANISM
 Takifugu rubripes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;

Tetraodontidae; Tetraodontidae; Takifugu.

1

Elgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,

Bouchireb,N., Cottage,A., Yeo,G.S., Umrana,Y., Williams,G. and

Brenner,S.

Generation and analysis of 25 Mb of genomic DNA from the pufferfish

Fugu rubripes by sequence scanning

Genome Res. 9 (10), 960-971 (1999)

99455097

10523524

2 (bases 1 to 593)

Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrana,Y.,

Williams,G. and Brenner,S.

Direct Submission

Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource

Centre Hinnton, Cambridge, CB10 1SB. Email: biohelp@hgmrc.ac.uk

Vector: pBluescript II KS

V type: phagemid

PRIMER: KS

DESCR:

One pass dye-terminator sequencing of cosmid cloned genomic

sequence.

Location/Qualifiers

1..593

/organism="Takifugu rubripes"

/mol_type="genomic DNA"

/db_xref="taxon:31033"

/clone="067111bD11"

/clone_lib="cosmid 067111"

ORIGIN

Query Match 66.4%; Score 18.6; DB 9; Length 593;

Best Local Similarity 80.8%; Pred. No. 1.1e+03;

Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAACCG 26

Db 46 AANATGCTGMAAGAGAGAGAGAGCG 71

CO300868

636 bp mRNA linear EST 25-JUN-2004

EK179552.5prime Exelixis FlyTag CK01 PCDNA-SK+ Drosophila

melanogaster CDNA clone EK179552 5, mRNA sequence.

CO300868

1 GI:49222564

EST.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 636)

Kopczynski,C., Platt,D., Campbell,J., Muzong,C., Laufer,A.,

Peterson,B. and Swimmer,C.

Exelixis FlyTag EST Project CK01 Library

Unpublished (2004)

Contact: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu

LOCUS	AI135620	642 bp	mRNA	linear	EST 02-DEC-2000
DEFINITION	GH13441.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH13441 5 similar to CG9322: FBan0009322				
GO: []	Located on: 3R 87F12-87F12:: 08/12/2002, mRNA sequence.				
ACCESSION	AI135620				
VERSION	AI135620.1	GI:3628178			
KEYWORDS	EST.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE	1 (bases 1 to 642)				
AUTHORS	Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.				
TITLE	BDGP/HMI Drosophila EST Project				
JOURNAL	Unpublished (2001)				
COMMENT	Other_ESTs: GH13441.3prime Contact: Stapleton, M. BDGP Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic AB003701: arm:3R [9357746,9566163] estimated-cyto:87F4-87F14: 04/10/2001 Plasmid: GH.134 row: D column: 5 High quality sequence stop: 593 POLYA=No.				
FEATURES	Location/Qualifiers				
source	1..642				
	/organism="Drosophila melanogaster"				
	/mol_type="mRNA"				
	/db_xref="taxon:7227"				
	/clone="GH13441"				
	/sex="male and female"				
	/dev_stage="adult"				
	/lab_host="DH5 - alpha"				
	/clone_lib="GH Drosophila melanogaster head pOT2"				
	/note="Organ: head; Vector: pOT2; Site:1: EcoRI; Site 2: XhoI; sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."				
ORIGIN					
Query Match	66.4%;	Score 18.6;	DB 1;	Length 642;	
Best Local Similarity	84.0%;	Pred. No. 1.1e+03;			
Matches	21;	Conservative	0;	Mismatches	4; Indels 0; Gaps 0;
QY	2	ATATGCTGAAACGCGAGAGAACCG	26		
Db	191	ATATGCTGAAACGCGAGAGAACCG	215		
RESULT 30					
CN882707					
LOCUS	CN882707	671 bp	mRNA	linear	EST 04-JUN-2004
DEFINITION	010812AASB003156HT (AASB) Royal Gala 10 DAFB fruit Malus x domestica cDNA clone AASB003156, mRNA sequence.				
ACCESSION	CN882707				
VERSION	CN882707.1	GI:48268949			
KEYWORDS	EST.				
SOURCE	Malus x domestica (cultivated apple)				
ORGANISM	Malus x domestica Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.				
REFERENCE	1 (bases 1 to 671)				
AUTHORS	Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., McCartney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.				
TITLE	HortResearch Apple EST Project				
JOURNAL	Unpublished (2004)				
COMMENT	Contact: Gleave,A. Sequencing Facility				
FEATURES	Location/Qualifiers				
source	1..640				
	/organism="Malus x domestica"				
	/mol_type="mRNA"				
	/db_xref="taxon:3750"				
	/clone="AARA008897"				
	/tissue_type="Leaf"				
	/dev_stage="partially senescing leaf"				
	/clone_lib="(AARA) Royal Gala partially senescing leaf"				
	/note="Vector: pBK-CMV; Library sequenced by Genesys Research & Development"				
ORIGIN					
Query Match	66.4%;	Score 18.6;	DB 7;	Length 640;	
Best Local Similarity	84.0%;	Pred. No. 1.1e+03;			
Matches	21;	Conservative	0;	Mismatches	4; Indels 0; Gaps 0;
QY	2	ATATGCTGAAACGCGAGAGAACCG	26		
Db	43	ATATCTGAAACGCGAGACACTG	67		
RESULT 29					
AI135620					

The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

FEATURES

source
1..671
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AASB003156"
/tissue_type="Young fruit"
/dev_stages="10 days after full bloom"
/clone_lib="(AASB) Royal Gala 10 DAFB fruit"
/note="Vector: pBluescript SK(-); Library sequenced by
Genesis Research & Development"

ORIGIN

Query Match 66.4%; Score 18.6; DB 7; Length 671;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAACCG 26

Db 49 ATATCCTGAACGCGAGAGACGCTG 73

RESULT 31

CN879811

LOCUS

DEFINITION 010419AASNA004412HT (AASA) Royal Gala 10 DAFB fruit Malus x domestica cDNA clone AASA004412, mRNA sequence.

VERSION CN879811

KEYWORDS EST.

SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosids; eucotsids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1 (bases 1 to 675)

AUTHORS Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave, A.

TITLE Sequencing Facility

JOURNAL The Horticulture and Food Research Institute of New Zealand Ltd

COMMENT 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand

Tel: 00 64 09 815 4200

Fax: 00 64 09 815 4201

Email: est@hortresearch.co.nz.

FEATURES

source
1..675
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AASA004412"
/tissue_type="Fruit"
/dev_stages="10 days after full bloom"
/clone_lib="(AASA) Royal Gala 10 DAFB fruit"
/note="Vector: pBluescript SK(-); Library sequenced by
Genesis Research & Development"

ORIGIN

Query Match 66.4%; Score 18.6; DB 7; Length 675;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAACCG 26

Db 60 ATATCCTGAACGCGAGAGACGCTG 84

RESULT 32

CN918097

LOCUS

DEFINITION 030203ABPB004660HT (ABPB) M9 root tips Malus x domestica cDNA clone ABPB004660, mRNA sequence.

ACCESSION CN918097

VERSION CN918097.1

KEYWORDS GI:48390597

SOURCE Malus x domestica (cultivated apple)

ORGANISM Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosids; eucotsids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1 (bases 1 to 683)

AUTHORS Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave, A.

TITLE Sequencing Facility

JOURNAL The Horticulture and Food Research Institute of New Zealand Ltd

COMMENT 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand

Tel: 00 64 09 815 4200

Fax: 00 64 09 815 4201

Email: est@hortresearch.co.nz.

FEATURES

source

1..683
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="ABPB004660"
/tissue_type="Root tips (distal 1.5 cm)"
/clone_lib="(ABPB) M9 root tips"
/note="Vector: pBluescript SK(-); Library sequenced by
Genesis Research & Development"

ORIGIN

Query Match 66.4%; Score 18.6; DB 7; Length 683;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAACCG 26

Db 1 ATATCCTGAACGCGAGAGACGCTG 25

RESULT 33

AQ657387/c

LOCUS

DEFINITION Sheared DNA-2N16.TR Sheared DNA Trypanosoma brucei genomic clone AQ657387, genomic survey sequence.

ACCESSION AQ657387

VERSION AQ657387.1

KEYWORDS GI:5165155

SOURCE GSS.

ORGANISM Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

REFERENCE 1 (bases 1 to 684)

AUTHORS El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Garrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library

Unpublished (1999)

Other GSSs: Sheared DNA-2N16.TF

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: nelsayed@tigr.org
 Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: <http://www.tigr.org/tdb/mdb/tbdb/>.
 Seq primer: M13-Reverse
 Class: shotgun.

FEATURES

source

1. .684
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927/4 GUTat 10.1"
 /db_xref="taxon:5691"
 /clone="Sheared DNA-2N16"
 /clone_lib="Sheared DNA"

/notes="Vector: pUC18; Site 1: SmaI; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Borell, Oxford University Press, 1999)."

ORIGIN

Query Match 66.4%; Score 18.6; DB 8; Length 684;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGCAGAGAAACC 25

||||| ||||| ||||| ||||| |||||
 Db 548 AATATCTGTAACCGCCCAATTAACC 524

RESULT 34

CL527496

LOCUS

DEFINITION 83k06rp42.f1 RPCI-42 Bos taurus genomic clone 83k06rp42, genomic survey sequence.

VERSION CL527496.1 GI:47120284

KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 799)

Aycock,M.M., Najjar,F.Z., Gasbarre,L.C., Van Tassel,C.P.,

Sonstegard,T.S., Conner,E.E., Capuco,A.V. and Roe,B.A.

Bovine BAC End Sequences from RPCI-42 Library

Unpublished (2004)

Contact: Bruce A. Roe

Advanced Center for Genome Technology

University of Oklahoma Department of Chemistry and Biochemistry

620 Parrington Oval, Room 208, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Class: BAC ends

High quality sequence start: 133

High quality sequence stop: 524.

FEATURES

source

1. .799
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="Holstein Bull"
 /db_xref="taxon:9913"
 /clone="83k06rp42"
 /sex="male"

/clone_lib="RPCI-42"
 /notes="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI"

Query Match 66.4%; Score 18.6; DB 9; Length 799;
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGCAGAGAAACCGCG 28

||||| ||||| ||||| ||||| |||||

Db 63 AGTAGNCNGNAACCGCAGAAACCACG 90

RESULT 35

CG016439

LOCUS

DEFINITION ZUAAG30TH ZM_3_0_4_0_KB Zea mays genomic clone ZMWBPa0006E11, genomic survey sequence.

ACCESSION CG016439

VERSION CG016439.1 GI:33888604

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 427)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,

Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,

Citek,R.W., Nummer,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: ZUAAG30TV

Contact: Cathy Whitelaw

TIGR

712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: Sheared ends.

FEATURES

source

1. .427
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMWBPa0006E11"
 /clone_lib="ZM_3_0_4_0_KB"
 /notes="Vector: pBCSK; Site_1: HincII; 3-4 kb 'unfiltered' genomic DNA library"

ORIGIN

Query Match 65.7%; Score 18.4; DB 9; Length 427;

Best Local Similarity 78.6%; Pred. No. 1.3e+03;

Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGCAGAGAAACCGCG 28

||||| ||||| ||||| ||||| |||||

Db 332 AATATGCTGCACGCTAGAGAGGCCG 359

RESULT 36

AQ724090/c

LOCUS

DEFINITION HS_5375_A2_H09 SP65 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=951 Col=18 Row=O, genomic survey sequence.

ACCESSION AQ724090

VERSION AQ724090.1 GI:5483759

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 456)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

TITLE
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE
99380589

PUBMED
10449764

COMMENT
Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Research Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 951 row: 0 column: 18

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 456.

Location/Qualifiers

FEATURES

source

1. 456

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clones="Plate:951 Col=18 Row=0"

/sex="male"

/clone_lib="RPCI-11 Human Male BAC Library"

/note="Vector: pBACe3.6; Site.1: EcoRI; Site.2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor

and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the

pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match 65.7%; Score 18.4; DB 8; Length 456;

Best Local Similarity 78.6%; Pred. No. 1.3e+03;

Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATGTGTTGAACGCGAGAGAACCGCG 28

|||||

Db 300 AATGTGTTACAGCGGTGAGAACCGCG 273

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Leads/Wash U Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Libraries were constructed by Dr. Stavros Bashiardes as part of the

Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and

Washington Univ. in St. Louis (USA) DNA sequencing by: Washington

University Genome Sequencing Center For information on obtaining a

clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)

Seq primer: -40RP from Gibco

High quality sequence stop: 416.

Location/Qualifiers

1. 496

/organism="Physcomitrella patens"

/mol_type="mRNA"

/db_xref="taxon:3218"

/clones="PEP_SOURCE_ID:PPN091205"

/tissue_type="protonemata: 7 day old tissue auxin treated"

/lab_host="DH10B"

/clone_lib="Moss EST library PPN"

/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:

XhoI; Construction of the cDNA library was carried out

using Stratagene 'UnizAP - cDNA synthesis kit'. cDNA was

constructed using an oligo dT primer/linker that contains

a XhoI site within it. Following ds cDNA synthesis,

EcoRI adapters were ligated to the blunt ends and sample

sticky end on one side and a XhoI sticky end on the other.

This cDNA was ligated directionally in UnizAP arms. The

vector is designed containing the pBluescript sequence as

well as lambda DNA and cDNA is cloned within this

pBluescript sequence. The vector was then packaged using

Gold gigapackaging extracts. Library was grown in XL1Blue

MRP cells and amplified. The library was excised by mass

excision using Stratagene 'Mass excision kit' that uses

exsist as a helper phage that releases the pBluescript

sequence and circularises it as single stranded plasmids

that are then packaged (by helper phage) and secreted out

of the host cell as phagemids. SOLR cells were transformed

with phagemids and the library was plated out on LB-amp

plates to select for transformants. Approximately

1,000,000 colonies were grown and recovered. The double

stranded plasmid library was recovered by using Qiaagen

Midi prep kit. 2 micro grams of each library were used to

transform DH10B cells by electroporation."

Query Match 65.7%; Score 18.4; DB 2; Length 496;

Best Local Similarity 78.6%; Pred. No. 1.3e+03;

Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATGTGTTGAACGCGAGAGAACCGCG 28

|||||

Db 372 AATTGTTGAACGCGGAGAGAACCGAG 399

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ORGANISM

REFERENCE

AUTHORS

Leads/Wash U Moss EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Libraries were constructed by Dr. Stavros Bashiardes as part of the

Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and

Washington Univ. in St. Louis (USA) DNA sequencing by: Washington

University Genome Sequencing Center For information on obtaining a

clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)

Seq primer: -40RP from Gibco

High quality sequence stop: 416.

Location/Qualifiers

1. 496

/organism="Physcomitrella patens"

/mol_type="mRNA"

/db_xref="taxon:3218"

/clones="PEP_SOURCE_ID:PPN091205"

/tissue_type="protonemata: 7 day old tissue auxin treated"

/lab_host="DH10B"

/clone_lib="Moss EST library PPN"

/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:

XhoI; Construction of the cDNA library was carried out

using Stratagene 'UnizAP - cDNA synthesis kit'. cDNA was

constructed using an oligo dT primer/linker that contains

a XhoI site within it. Following ds cDNA synthesis,

EcoRI adapters were ligated to the blunt ends and sample

sticky end on one side and a XhoI sticky end on the other.

This cDNA was ligated directionally in UnizAP arms. The

vector is designed containing the pBluescript sequence as

well as lambda DNA and cDNA is cloned within this

Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Rigggs,F., de Jong,P. and Fraser,C.M.
 Rat BAC End Sequences from Library CHORI-230 MboI segment
 Unpublished (1999)
 Other GSSs: CH230-39416.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (<http://www.chori.org/bacpac/oreringinformation.htm>). BAC end
 page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html
 Plate: 394 row: I column: 6
 Seq primer: SP6
 Class: BAC ends.

FEATURES

source
 1. .582
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="Genomic DNA"
 /strain="BN/SeNHsd/MCW"
 /db_xref="taxon:10116"
 /clones="CH230-39416"
 /sex="Female"
 /cell_type="Brain"
 /clone_lib="CHORI-230 Segment 2"
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
 CHORI-230 Rat (BN/SeNHsd/MCW) BAC library produced by
 Pieter de Jong"

ORIGIN

Query Match 65.7%; Score 18.4; DB 8; Length 582;
 Best Local Similarity 78.6%; Pred. No. 1.3e+03;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 Db 363 ACTCTGCTGATAGCAAGAGAAACCGCG 336

RESULT 39
 CB020289
 LOCUS
 DEFINITION
 CB020289.y1 Haemonchus contortus intestine SL2 TOPO v1 Haemonchus
 contortus cDNA 5' similar to TR:045812 O45812 T23G11.9 PROTEIN. [1]
 i, mRNA sequence.

ACCESSION
 VERSION
 CB020289.1 GI:27595025
 EST

KEYWORDS

SOURCE
 Haemonchus contortus

ORGANISM
 Haemonchus contortus

REFERENCE
 1 (bases 1 to 655)

AUTHORS
 McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
 Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
 Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
 Tagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
 Harwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
 McCann,R., Waterston,R. and Wilson.R.

The Washington Univ. Nematode EST Project, 1999

Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Claire Murphy and Dr. James McCarter
 at Washington University, St. Louis. Oligo(dT)-SL2 PCR based
 library. cDNA PCR products of size >400 nucleotides containing SL2
 on the 5' end and oligo(dT) on the 3' end were non-directionally
 cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning
 protocol. Intestine RNA was provided by Dr. Douglas Jasmier of
 Washington State University (djasmier@vetmed.wsu.edu).
 Seq primer: SL1 primer
 High quality sequence stop: 525.

FEATURES

source
 1. .655
 Location/Qualifiers
 /organism="Haemonchus contortus"
 /mol_type="mRNA"
 /db_xref="taxon:6289"
 /tissue_type="intestine"
 /lab_host="DH10B"
 /clone_lib="Haemonchus contortus intestine SL2 TOPO v1"
 /note="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;
 Site 2: EcoRI; The library was constructed by Claire
 Murphy and Dr. James McCarter at Washington University,
 St. Louis. Oligo(dT)-SL2 PCR based library. cDNA PCR
 products of size >400 nucleotides containing SL2 on the 5'
 end and oligo(dT) on the 3' end were non-directionally
 cloned into pCRII-TOPO(Invitrogen) following the Topo TA
 cloning protocol. Intestine RNA was provided by Dr.
 Douglas Jasmier of Washington State University
 (djasmier@vetmed.wsu.edu)."

ORIGIN

Query Match 65.7%; Score 18.4; DB 6; Length 655;
 Best Local Similarity 78.6%; Pred. No. 1.3e+03;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 Db 264 ATTTGCTGATGCGGAGAGAAACCGCG 291

RESULT 40
 BH100535/c

LOCUS

DEFINITION
 BH100535
 BH100535
 BH100535.1 GI:14924482

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 672)

REFERENCE

AUTHORS

Zhao,S., Nierman,M., Malek,J., Shvartsbeyn,A., Gebregorgis,E.,

Russell,D., de Jong,P. and Fraser,C.M.

Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

Other GSSs: RPCI-24-333F21.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

library availability, please contact Pieter de Jong

(pdejong@mail.cho.org). Clones may be purchased from BACPAC

Resources (<http://www.chori.org/bacpac/orderingframe.htm>). BAC end

page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html

Plate: 333 row: F column: 21

Seq primer: T7

```

vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"

ORIGIN
Query Match      65.7%; Score 18.4; DB 6; Length 675;
Best Local Similarity 78.8%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AATATGCTGAAACGCGAGAGAAACCGCG 28
      |||||
DB      581 ATTATGCTGAACTCGAGAGAACTGGG 608
      |||||

RESULT 42
BH929269/c
LOCUS
DEFINITION
  BH929269          695 bp      DNA      linear      GSS 01-OCT-2002
  od181f08.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
  sequence.
ACCESSION
  BH929269
VERSION
  BH929269.1 GI:23409335
KEYWORDS
  GSS.
SOURCE
  Brassica oleracea
  Brassica oleracea
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eustosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 695)
  Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
  Nash,W., Rabinowicz,P.D. and Wilson,R.K.
  Whole genome shotgun reads from Brassica oleracea
  Unpublished (2002)
  Contact: Richard K. Wilson
  Genome Sequencing Center
  Washington University School of Medicine
  Email: submissions@watson.wustl.edu
  Plate: od181 row: f column: 08
  Seq primer: -38RPpOT reverse
  Class: shotgun
  High quality sequence start: 32
  High quality sequence stop: 513.
  Location/Qualifiers
    1..695
      /organism="Brassica oleracea"
      /mol_type="genomic DNA"
      /db_xref="taxon:3712"
      /clone_lib="B.oleracea002"
      /note="Vector: pOTw13; Whole genome shotgun library from
      flowering buds. DNA was purified from a crude nuclear
      prep using Brassica oleracea T01000DH3 buds provided by
      Thomas Osborn at the University of Wisconsin. Genomic
      DNA was provided by Pablo Rabinowicz (SSH) and the
      shotgun library prepared at Washington University Genome
      Sequencing Center."

ORIGIN
Query Match      65.7%; Score 18.4; DB 8; Length 695;
Best Local Similarity 78.8%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AATATGCTGAAACGCGAGAGAAACCGCG 28
      |||||
DB      162 AAATGCCGACACGCGAGCAAAACCGCG 135
      |||||

RESULT 43
BH549312/c
LOCUS
DEFINITION
  BH549312          697 bp      DNA      linear      GSS 14-DEC-2001
  BOHEP93TR BOHE Brassica oleracea genomic clone BOHEP93, genomic
  survey sequence.
ACCESSION
  BH549312
VERSION
  BH549312.1 GI:117801092
KEYWORDS
  GSS.

```



```

SOURCE
ORGANISM
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 697)
TOWN,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOHEP93TF
Contact: Chris Town
TIGR Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..697
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TOL000H3"
/db_xref="taxon:3712"
/clone="BOHEP93"
/clone_lib="BOHE"
/note="Vector: pHS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHS1 using BstXI linkers"

ORIGIN
Query Match 65.7%; Score 18.4; DB 8; Length 697;
Best Local Similarity 78.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 588 AAAATGCCAACACGCGACGAGAACCGCG 561

RESULT 44
CK326303 743 bp mRNA linear EST 17-DEC-2003
LOCUS Hd mx23_03A06.T7 Hypsibius dujardini mixed stage 5'capped (fraction
3) Hypsibius dujardini cDNA clone Hd mx23_03A06 5' similar to
Q99JR7 (Q99JR7) RIKEN cDNA 2610012022 gene, mRNA sequence.
ACCESSION CK326303.1 GI:39999894
VERSION EST.
KEYWORDS Hypsibius dujardini
SOURCE Hypsibius dujardini
ORGANISM Eukaryota; Metazoa; Tardigrada; Eutardigrada; Apochela;
Hypsibiidae; Hypsibius.
REFERENCE
1 (bases 1 to 743)
Daub,J., Thomas,F., Aboobaker,A. and Blaxter,M.L.
A survey of genes expressed in the tardigrade Hypsibius dujardini
Unpublished (2003)
JOURNAL Contact: Blaxter ML
COMMENT Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
3JT, UK.
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
PCR Primers
FORWARD: M13R
BACKWARD: M13L
Plate: 03 row: A column: 06
Seq primer: T7 (TAATACGACTCACTATAGGG)
High quality sequence stop: 481.
Location/Qualifiers
1..743

FEATURES
source
/organism="Hypsibius dujardini"
/mol_type="mRNA"
/db_xref="taxon:232323"
/clone="Hd mx23_03A06"
/sex="parthenogenic"
/tissue_type="whole body"
/dev_stage="mixed (adult and juvenile)"
/fraction 3)
/note="Vector: pSPORT1; Site 1: Sal I (5'end); Site 2: Not
I (3'end); Tardigrades (also know as water bears) are
small free living animals inhabiting marine, fresh water
and water film habitats. Hypsibius dujardini is a
freshwater species maintained in lab culture (source
strain Sciento 2151). The library was prepared from adults
and juveniles and was constructed in pSPORT1 vector
(Superscript, Invitrogen) using GeneRacer (Invitrogen)
purified 5'capped mRNA by Jennifer Daub, University of
Edinburgh. Sequencing was performed by Frances Thomas,
University of Edinburgh."

ORIGIN
Query Match 65.7%; Score 18.4; DB 7; Length 743;
Best Local Similarity 78.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 230 AAAATGCCGAATCCAAGCGAACCAGCG 257

RESULT 45
BE615972 750 bp mRNA linear EST 24-AUG-2000
LOCUS 601279483F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611516 5',
DEFINITION mRNA sequence.
ACCESSION BE615972
VERSION BE615972.1 GI:9897658
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 750)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM269 row: e column: 21
High quality sequence stop: 551.
Location/Qualifiers
1..750
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3611516"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_39"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA"

FEATURES
source

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AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc..
CDNA Library Preparation: CLONETECH Laboratories, Inc..
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LILAM1144 row: e column: 08
High quality sequence start: 174
High quality sequence stop: 509.

FEATURES
source Location/Qualifiers
1..790 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cclone="IMAGE:4294639"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: Sfil (ggcgctctggcc); Site 2: Sfil (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGAGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN
Query Match 65.7%; Score 18.4; DB 2; Length 790;
Best Local Similarity 95.0%; Pred.No.1.4e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ATGCTGAACGCGAGAGAAA 23
||||| ||||| ||||| |||||
Db 270 ATGCTGAACGTGAGAGAAA 289

RESULT 49
BI753870

LOCUS BI753870 792 bp mRNA linear EST 25-SEP-2001
DEFINITION 603027558F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5197791 5', mRNA sequence.

ACCESSION BI753870
VERSION BI753870.1 GI:15745448
KEYWORDS EST.
SOURCE BI753870.1 Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 792)

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc..
CDNA Library Preparation: Life Technologies, Inc..
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11495 row: d column: 16
High quality sequence stop: 761.

FEATURES
Location/Qualifiers

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